

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:34:14 ; Search time 46 Seconds
(without alignments)
902.243 Million cell updates/sec

Title: US-10-749-075-2

Perfect score: 2703

Sequence: 1 MRCSPGVWLAASLLHVS.....TIGILMSAPNFVEANSKDFSA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	502	2	US-08-771-737-2
2	2703	100.0	502	2	US-09-954-936-2
3	2698	99.8	502	1	US-08-466-589-8
4	2698	99.8	502	1	US-08-700-636-8
5	2698	99.8	502	2	US-08-467-574-8
6	2698	99.8	502	2	US-09-217-345-8
7	2698	99.8	502	2	US-08-487-596-12
8	2698	99.8	502	2	US-09-892-985-8
9	2698	99.8	502	2	US-09-579-250-2
10	2698	99.8	502	2	US-09-703-951A-12
11	2692	99.6	502	2	US-09-579-250-10
12	2688	99.4	502	2	US-09-579-250-12
13	2682	99.2	502	2	US-09-579-250-14
14	2540	94.0	502	1	US-08-278-635B-7
15	2540	94.0	502	2	US-08-464-258B-7
16	2540	94.0	502	2	US-08-471-961-7
17	2540	94.0	502	2	US-09-345-109C-7
18	2022	74.8	446	2	US-08-660-451A-12
19	1816.5	67.2	511	1	US-08-278-635B-8
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22	1816.5	67.2	511	2	US-09-345-109C-8
23	1474.5	54.6	470	2	US-09-579-250-6
24	1254.5	46.4	501	2	US-09-303-232C-6
25	1242	45.9	496	2	US-09-303-232C-4
26	1155.5	42.7	770	2	US-09-303-232C-2
27	945	35.0	529	1	US-08-496-855A-2

28	945	35.0	529	2	US-08-487-596-2	Sequence 2, Appli
29	945	35.0	529	2	US-08-660-451A-2	Sequence 2, Appli
30	945	35.0	529	2	US-09-703-951A-2	Sequence 2, Appli
31	943	34.9	510	1	US-08-278-635B-4	Sequence 4, Appli
32	943	34.9	510	2	US-08-471-961-4	Sequence 4, Appli
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34	940.5	34.8	511	2	US-08-464-258B-4	Sequence 4, Appli
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36	920.5	34.1	528	1	US-08-466-589-2	Sequence 2, Appli
37	920.5	34.1	528	1	US-08-700-636-2	Sequence 2, Appli
38	920.5	34.1	528	2	US-08-467-574-2	Sequence 2, Appli
39	920.5	34.1	528	2	US-09-217-345-2	Sequence 2, Appli
40	920.5	34.1	528	2	US-09-892-985-2	Sequence 2, Appli
41	920	34.0	607	2	US-09-949-016-7817	Sequence 7817, Ap
42	916	33.9	627	2	US-08-660-451A-6	Sequence 6, Appli
43	908	33.6	504	1	US-08-466-589-4	Sequence 4, Appli
44	908	33.6	504	1	US-08-700-636-4	Sequence 4, Appli
45	908	33.6	504	2	US-08-467-574-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-771-737-2
; Sequence 2, Application US/08771737
; Patent No. 6323000

; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.

; APPLICANT: Gopalakrishnan, Murali

; APPLICANT: McKenna, David G.

; APPLICANT: Monteggia, Lisa M.

; APPLICANT: Roch, Jean-Marc

; APPLICANT: Sullivan, James P.

; APPLICANT: Touma, Edward

; APPLICANT: Abbott Laboratories

; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE

; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF

; FILE REFERENCE: 6017.US.01

; CURRENT APPLICATION NUMBER: US/08/771,737

; CURRENT FILING DATE: 1996-12-20

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 502

; TYPE: PRT

; ORGANISM: homo sapien

US-08-771-737-2

Query Match 100.0%; Score 2703; DB 2; Length 502;

Best Local Similarity 100.0%; Pred. No. 4.1e-274;

Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRCSPGVWLAASLLHVS	LOGEFQRLKLVKNYNPLRPVANDS	QPLTVYFSLSL 60
Db	1	MRCSPGVWLAASLLHVS	LOGEFQRLKLVKNYNPLRPVANDS	QPLTVYFSLSL 60
QY	61	QIMDVDEKNQVLTINWLQMS	WDHYLQWNSEYFGVKTVPDQGI	WKPDILLYNSADE 120
Db	61	QIMDVDEKNQVLTINWLQMS	WDHYLQWNSEYFGVKTVPDQGI	WKPDILLYNSADE 120
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Db	121	RFDAFTHTNVLNNSGHCQYL	PPGIFKSSCYIDVRFPDVQHC	KLKFGSWSYGGSLDL 180
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Db 301 MIIVGLSVVTVVLQVHHHDPGGKMPKWKTRVILLNWCAWFLMRKRPGBDKVRPACQHK 360
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Db 361 QRCRSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDDPLAKLIEVRVIANRFRCDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDDPLAKLIEVRVIANRFRCDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 2
US-09-954-936-2
; Sequence 2, Application US/09954936
; Patent No. 6683157
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A. Murali
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017 US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match 100.0%; Score 2703; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.1e-274;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKYNPLERPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKYNPLERPVANDSQPLTVYFSL 60
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Db 121 RFDATHTNVLNVSNGHCQVLPPIKSSCYIDVRWPPDVQHCCLKFGSWSYGGWSLDL 180
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Db 181 QMQEADISGYPNGEWDLVGIPGRSERFYECCKEPYPDVTFVTVMRRRTLYGLNLLIP 240
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Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
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Db 301 MIIVGLSVVTVVLQVHHHDPGGKMPKWKTRVILLNWCAWFLMRKRPGBDKVRPACQHK 360

QY 361 QRCRSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCRSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDDPLAKLIEVRVIANRFRCDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDDPLAKLIEVRVIANRFRCDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 3
US-08-466-589-8
; Sequence 8, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-466-589-8

Query Match 99.8%; Score 2698; DB 1; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKYNPLERPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
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Db 241 CVLISALALAVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
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Db 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
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Db 421 LHGGQPEGDPDLAKLILEVRYIANRFRCDSEAVCESEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4

US-08-700-636-8
; Sequence 8, Application US/08700636
; Patent No. 5916582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen B.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-700-636-8

Query Match 99.8%; Score 2698; DB 1; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRCSPGCVWLAAASLLHVSLOGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGCVWLAAASLLHVSLOGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
Qy 61 QIMDVDEKQVLTNNIWLQMSWTDDHYLQNVSEYPOKTVRPPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNNIWLQMSWTDDHYLQNVSEYPOKTVRPPDGOIWKPDILLYNSADE 120
Qy 121 RPDATFHTNVLNSSGHCQYLPFGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
Db 121 RPDATFHTNVLNSSGHCQYLPFGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
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Db 181 QMEADISGYPNGEWDLVGIPGKRSRFEYCKEKPYPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALAVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALAVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
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Db 301 MIIVGLSVVVTVVLQYHHDDPDGKMPKWTIRVILLNWCWFLRMKRPBGDKVRPACQHK 360
Qy 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Db 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Qy 421 LHGGQPEGDPDLAKLILEVRYIANRFRCDSEAVCESEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPEGDPDLAKLILEVRYIANRFRCDSEAVCESEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5

US-08-467-574-8
; Sequence 8, Application US/08467574
; Patent No. 6022704
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,574
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:

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/ NAME: Seidman, Stephanie L
/ REGISTRATION NUMBER: 33,779
/ REFERENCE/DOCKET NUMBER: 6362-9949
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-238-0999
/ TELEFAX: 619-238-0062
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 502 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
US-08-467-574-8

Query Match          99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNOVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDGOIQWKPDI 120
DB 61 QIMDVDEKNOVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDGOIQWKPDI 120
QY 121 RFDAFTHTNVLVNSSGHCQYLPFGIFPKSSCYIDVRWFPFDVQHCCLKFGS 180
DB 121 RFDAFTHTNVLVNSSGHCQYLPFGIFPKSSCYIDVRWFPFDVQHCCLKFGS 180
QY 121 RFDAFTHTNVLVNSSGHCQYLPFGIFPKSSCYIDVRWFPFDVQHCCLKFGS 180
DB 121 RFDAFTHTNVLVNSSGHCQYLPFGIFPKSSCYIDVRWFPFDVQHCCLKFGS 180
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DB 181 QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTMRRRTLY 240
QY 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVPLIA 300
DB 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVPLIA 300
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DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEVK 360
QY 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPPTDPSGVVCGRM 420
DB 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPPTDPSGVVCGRM 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRCODESEAVCSEWKFAACVVDRLCL 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRCODESEAVCSEWKFAACVVDRLCL 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
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RESULT 6

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US-09-217-345-8
Sequence 8, Application US/09217345
Patent No. 6303753
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & Mcauliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
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/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/217,345
/ FILING DATE: 21-DEC-98
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/467,574
/ FILING DATE: 05-JUN-95
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/466,589,
/ FILING DATE: 05-JUN-95
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/028,031
/ FILING DATE: 08-MAR-93
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seidman, Stephanie L
/ REGISTRATION NUMBER: 33,779
/ REFERENCE/DOCKET NUMBER: 24735-9949B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-450-8400
/ TELEFAX: 619-587-5360
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 502 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
US-09-217-345-8
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Query Match          99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSL 60
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DB 61 QIMDVDEKNOVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDGOIQWKPDI 120
QY 121 RFDAFTHTNVLVNSSGHCQYLPFGIFPKSSCYIDVRWFPFDVQHCCLKFGS 180
DB 121 RFDAFTHTNVLVNSSGHCQYLPFGIFPKSSCYIDVRWFPFDVQHCCLKFGS 180
QY 181 QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTMRRRTLY 240
DB 181 QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTMRRRTLY 240
QY 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVPLIA 300
DB 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVPLIA 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEVK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEVK 360
QY 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPPTDPSGVVCGRM 420
DB 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPPTDPSGVVCGRM 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRCODESEAVCSEWKFAACVVDRLCL 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRCODESEAVCSEWKFAACVVDRLCL 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
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Db 481 ICTIGILMSAPNFVEAVSKDFA 502
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RESULT 7
US-08-487-596-12
; Sequence 12, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-487-596-12
Query Match 99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGVWLAASLIHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGVWLAASLIHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKQVLTNIWLSQSWTDHYLQWNVSEYGVKTVRFPDGGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNIWLSQSWTDHYLQWNVSEYGVKTVRFPDGGQIWKPDILLYNSADE 120

QY 121 RPDATHTTNVLSNSSCHCOYLPPIFKSSCYIDVRHFPDVOHQCKLKFGSWSYGGHSLDL 180
Db 121 RPDATHTTNVLSNSSCHCOYLPPIFKSSCYIDVRHFPDVOHQCKLKFGSWSYGGHSLDL 180
QY 181 QMOEADISGYPNGEWDLVGIPGKRSERFVECCCKEPYDPVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMOEADISGYPNGEWDLVGIPGKRSERFVECCCKEPYDPVTFVTWRRRTLYYGLNLLIP 240
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Db 241 CVLISALALLVFLLPADSGEKISLITVLLSLTTFMLLVAEIMPATSDSVPLIAQVFAST 300
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Db 301 MIIVGLSVVVTYVLYQYHHDDPGGKMPKWRVILLNWCANFLMRKPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEVRYIANRFRQDSEAVCSWKFAACVVDRICLMAFSVFTI 480
Db 421 LHGGQPEGDPDLAKILEVRYIANRFRQDSEAVCSWKFAACVVDRICLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 8
US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-JUN-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 8:		Best Local Similarity 99.8%; Pred. No. 1.4e-273;		Best Local Similarity 99.8%; Pred. No. 1.4e-273;	
; SEQUENCE CHARACTERISTICS:		; LENGTH: 502 amino acids		Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
; TYPE: amino acid		; STRANDEDNESS: single		QY 1 MRCSPGGVWLAALASLLHVSLOGEFORKLYKELVKNNPLERPVANDSOPLTIVYFSLSL 60	
; TOPOLOGY: unknown		; MOLECULE TYPE: protein		Db 1 MRCSPGGVWLAALASLLHVSLOGEFORKLYKELVKNNPLERPVANDSOPLTIVYFSLSL 60	
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:		; QUERY MATCH		QY 61 QIMDVEKNQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120	
US-09-892-985-8		; Query Match		Db 61 QIMDVEKNQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120	
		; Best Local Similarity 99.8%; Pred. No. 1.4e-273;		QY 121 RPDATFHTNVLNNSGHCQYLPFGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180	
		; Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		Db 121 RPDATFHTNVLNNSGHCQYLPFGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180	
		QY 1 MRCSPGGVWLAALASLLHVSLOGEFORKLYKELVKNNPLERPVANDSOPLTIVYFSLSL 60		QY 181 QMOEADISGYPNGEWDLVGIPGKRSERFEYCKEYPDPVTFVTVMRRRTLYYGLNLLIP 240	
		Db 1 MRCSPGGVWLAALASLLHVSLOGEFORKLYKELVKNNPLERPVANDSOPLTIVYFSLSL 60		Db 181 QMOEADISGYPNGEWDLVGIPGKRSERFEYCKEYPDPVTFVTVMRRRTLYYGLNLLIP 240	
		QY 61 QIMDVEKNQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120		QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300	
		Db 61 QIMDVEKNQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120		Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300	
		QY 121 RPDATFHTNVLNNSGHCQYLPFGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180		QY 301 MIIVGLSVVTVIQLYHHDDPGGKMPKWTVRVILLNWCWFLRMKRPGEKVRPACQHK 360	
		Db 121 RPDATFHTNVLNNSGHCQYLPFGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180		Db 301 MIIVGLSVVTVIQLYHHDDPGGKMPKWTVRVILLNWCWFLRMKRPGEKVRPACQHK 360	
		QY 181 QMOEADISGYPNGEWDLVGIPGKRSERFEYCKEYPDPVTFVTVMRRRTLYYGLNLLIP 240		QY 361 QRCRSIASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420	
		Db 181 QMOEADISGYPNGEWDLVGIPGKRSERFEYCKEYPDPVTFVTVMRRRTLYYGLNLLIP 240		Db 361 QRCRSIASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420	
		QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300		QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480	
		Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300		Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480	
		QY 301 MIIVGLSVVTVIQLYHHDDPGGKMPKWTVRVILLNWCWFLRMKRPGEKVRPACQHK 360		QY 481 ICTIGILMSAPNFVEAVSKDFA 502	
		Db 301 MIIVGLSVVTVIQLYHHDDPGGKMPKWTVRVILLNWCWFLRMKRPGEKVRPACQHK 360		Db 481 ICTIGILMSAPNFVEAVSKDFA 502	
		QY 361 QRCRSIASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420		RESULT 9	
		Db 361 QRCRSIASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420		US-09-579-250-2	
		QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480		; Sequence 2, Application US/09579250	
		Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480		; Patent No. 6693172	
		QY 481 ICTIGILMSAPNFVEAVSKDFA 502		; GENERAL INFORMATION:	
		Db 481 ICTIGILMSAPNFVEAVSKDFA 502		; APPLICANT: Groppi, Vincent	
				; APPLICANT: Wolfe, Mark L.	
				; APPLICANT: Berkenpas, Mitchell B	
				; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel	
				; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists	
				; CURRENT FILING DATE: 2000-05-25	
				; NUMBER OF SEQ ID NOS: 14	
				; SOFTWARE: PatentIn Ver. 2.1	
				; SEQ ID NO 2	
				; LENGTH: 502	
				; TYPE: PRT	
				; ORGANISM: Homo sapiens	
				US-09-579-250-2	
				Query Match	
				99.8%; Score 2698; DB 2; Length 502;	

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; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohli, Vincent
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: SD99511A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3889
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-703-951A-12

Query Match          99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRCSPGGWMLAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
Db 1 MRCSPGGWMLAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
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Qy 121 RFDATFTNVLNVSNGHCQVLPFGIFKSSCYIDVRWFPFDVQHCCKLFGSWSYGGWSL 180
Db 121 RFDATFTNVLNVSNGHCQVLPFGIFKSSCYIDVRWFPFDVQHCCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYF 300
Db 241 CVLISALALLVFLLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYF 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Qy 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 12
US-09-579-250-12
; Sequence 12, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Mark L.
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12

Query Match          99.6%; Score 2692; DB 2; Length 502;
Best Local Similarity 99.6%; Pred. No. 5.8e-273;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRCSPGGWMLAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
Db 1 MRCSPGGWMLAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKQVLTNTIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Qy 121 RFDATFTNVLNVSNGHCQVLPFGIFKSSCYIDVRWFPFDVQHCCKLFGSWSYGGWSL 180
Db 121 RFDATFTNVLNVSNGHCQVLPFGIFKSSCYIDVRWFPFDVQHCCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYF 300
Db 241 CVLISALALLVFLLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYF 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Qy 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 12
US-09-579-250-12
; Sequence 12, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Mark L.
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
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; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-579-250-12

Query Match          99.4%; Score 2688; DB 2; Length 502;
Best Local Similarity 99.4%; Pred. No. 1.5e-272;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNNPLERPVANDSOPLTVYFSLSL 60
DB 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNNPLERPVANDSOPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPPDGGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPPDGGQIWKPDILLYNSADE 120
QY 121 RPDATFHTNVLNNSGHCQYLPPIFKSSCYIDVRWFFDVQVHCKLKFGSWSYGGWSL 180
DB 121 RPDATFHTNVLNNSGHCQYLPPIFKSSCYIDVRWFFDVQVHCKLKFGSWSYGGWSL 180
QY 181 QMOEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
DB 181 QMOEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 SVLISALALLVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCANFLMKRPGEDKVRPACQHK 360
DB 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCANFLMKRPGEDKVRPACQHK 360
QY 361 QRCRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
DB 361 QRCRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 13
US-09-579-250-14
; Sequence 14, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Mark L.
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-579-250-14

Query Match          99.2%; Score 2682; DB 2; Length 502;
Best Local Similarity 99.4%; Pred. No. 6.5e-272;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNNPLERPVANDSOPLTVYFSLSL 60
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DB 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNNPLERPVANDSOPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPPDGGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPPDGGQIWKPDILLYNSADE 120
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DB 121 RPDATFHTNVLNNSGHCQYLPPIFKSSCYIDVRWFFDVQVHCKLKFGSWSYGGWSL 180
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DB 181 QMOEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 SVLISALALLVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCANFLMKRPGEDKVRPACQHK 360
DB 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCANFLMKRPGEDKVRPACQHK 360
QY 361 QRCRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
DB 361 QRCRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 14
US-08-278-635B-7
; Sequence 7, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOVHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FRIEDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
```


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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:26:24 ; Search time 188 Seconds
(without alignments)
1173.235 Million cell updates/sec

Title: US-10-749-075-2

Perfect score: 2703

Sequence: 1 MRCSPGVWLAAALHVS.....TIGILMSAPNFVRAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	502	2	Aaw69216 V274T var
2	2698	99.8	502	2	Aaw44153 Human neu
3	2698	99.8	502	2	Aaw09025 Neuronal
4	2698	99.8	502	3	Aab24088 Human PRO
5	2698	99.8	502	4	Aab82690 Nicotinic
6	2698	99.8	502	4	Aab50012 Wild-type
7	2698	99.8	502	5	Abg70492 Human neu
8	2698	99.8	502	5	Abb82435 Human neu
9	2698	99.8	502	7	Ada10874 Human neu
10	2698	99.8	502	7	Ada47051 Human Pro
11	2698	99.8	502	7	Ades7310 Human Pro
12	2698	99.8	502	7	Adm68431 Human nic
13	2698	99.8	502	9	Aeb90709 Human alp
14	2698	99.8	515	9	Aec01800 Alpha-7 n
15	2693	99.6	502	8	Ades2166 Human alp
16	2692	99.6	502	4	Aab50015 Mutant hu
17	2690	99.5	502	7	Adk52598 Hematolog
18	2690	99.5	502	8	Adsl7052 Human 837
19	2690	99.5	502	8	Adr88593 Human alp
20	2688	99.4	502	4	Aab50016 Mutant hu
21	2682	99.2	502	4	Aab50017 Mutant hu
22	2675	99.0	502	8	Adr47549 Rhesus mo
23	2675	99.0	502	8	Adr47553 Rhesus mo
24	2675	99.0	502	9	Aeb90713 Macaca mu

25	2670	98.8	502	8	Ades2189 Rhesus mo
26	2670	98.8	502	8	Adr47551 Rhesus mo
27	2547	94.2	502	9	Aeb90707 Rat alpha
28	2546	94.2	502	9	Aeb90711 Mouse alp
29	2543	94.1	502	9	Aeb90722 Rat alpha
30	2542	94.0	502	8	Ades2172 Rat alpha
31	2536	93.8	499	9	Aeb90715 Bos tauru
32	2531	93.6	502	7	Ades7308 Rat Prote
33	2531	93.6	502	7	Ad47049 Rat Prote
34	2522.5	93.3	531	8	Adrl5995 Spline va
35	2429	89.9	502	2	Aaw12368 Neuronal
36	2429	89.9	502	9	Aeb90717 Chicken a
37	2073.5	76.7	509	9	Aeb90719 Zebra fis
38	2022	74.8	446	7	Ada10865 Human neu
39	2018	74.7	446	7	Adm68422 Human nic
40	1816.5	67.2	511	2	Aaw12369 Neuronal
41	1790	66.2	349	5	Abp69081 Human pol
42	1474.5	54.6	440	4	Aab50014 Chimeric
43	1360.5	50.3	448	4	Aab50018 Mature ce
44	1344	49.7	246	9	Aeb19062 Human nic
45	1254.5	46.4	501	3	Aay50816 H. viresc

ALIGNMENTS

RESULT 1

Aaw69216

ID Aaw69216 standard; protein; 502 AA.

XX Aaw69216;

DT 09-OCT-1998 (first entry)

DE V274T variant human alpha7 nACHR protein.

XX Alpha7 nACHR; alpha7 nicotinic acetylcholine receptor subunit; cancer;
neurodegeneration; enzyme dysfunction; affective disorder; therapy;
immune dysfunction; diabetic neuropathy; Alzheimer's disease;
schizophrenia.

OS Homo sapiens.

PN WO9828331-A2.

XX 02-JUL-1998.

PD 22-DEC-1997; 97WO-US023405.

PR 20-DEC-1996; 96US-00771737.

XX (ABBO) ABBOTT LAB.

PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM, Roch J;

PI Sullivan JP, Touma E;

DR WPI; 1998-377593/32.

XX N-PSDB; AAV44687.

PT Nucleic acid encoding variant of human alpha 7 nicotinic acetyl-choline
receptor sub-unit - used to identify modulators of the receptor,
potentially useful for treating neuro-degeneration, cancer etc.

Claim 15; Fig 2; 44pp; English.

CC This sequence is the V247T variant of human alpha7 nicotinic
acetylcholine receptor (nACHR) subunit of the invention. Cells containing
the DNA are used to express the protein and to identify modulators of
alpha7 nACHR activity or cytoprotective agents, e.g. antisense compounds
or antagonists that are potentially useful for treating
neurodegeneration, enzyme dysfunction, affective disorders and immune
dysfunction, such as cancer, post-herpetic neuralgia, diabetic
neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,

CC psychosis and schizophrenia. Probes based on the DNA are used to detect
CC the DNA in usual hybridization or amplification tests, while monoclonal
CC antibodies are used to detect the protein for diagnosis (in vitro or by
CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
CC the protein has about 100-fold greater sensitivity to cholinergic
CC receptor agonists (nicotine or acetylcholine) and response to these
CC agonists decays more slowly, but the wild-type inward rectification is
XX retained
SQ Sequence 502 AA;

Query Match 100.0%; Score 2703; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 7e-263;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60

QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RFDATEHTNVLVNSGHCQYLPPIGPKSCYIDVRWPFPPDVQHCXKFKGWSYGGWSLDL 180
DB 121 RFDATEHTNVLVNSGHCQYLPPIGPKSCYIDVRWPFPPDVQHCXKFKGWSYGGWSLDL 180

QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECKEYPDVTFTVTRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECKEYPDVTFTVTRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVTVLQYHHDDPGGKVPKWTRVILLNWCWFLMRKRPGEKVVPACQHK 360
DB 301 MIIVGLSVVTVTVLQYHHDDPGGKVPKWTRVILLNWCWFLMRKRPGEKVVPACQHK 360

QY 361 QRCRLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRCRLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTTPDSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPEGDPDLAKLILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGDPDLAKLILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2
AAW44153
ID AAW44153 standard; protein; 502 AA.
AC AAW44153;
XX AAW44153;
DT 14-MAY-1998 (first entry)
XX
DE Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
XX Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
KW Human; neuronal nicotinic acetylcholine receptor; NACHR; antibody.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..23 /label= signal
FT Domain 229..256 /label= TMD1
FT /note= "transmembrane domain"
FT

FT Domain 262..284
FT /label= TMD2
FT /note= "transmembrane domain"
FT Domain 290..317
FT /label= TMD3
FT /note= "transmembrane domain"
FT Domain 318..461
FT /label= cytoplasmic_loop
FT Misc-difference 343
FT /note= "encoded by CTS"
FT Domain 462..487
FT /label= TMD4
FT /note= "transmembrane domain"
XX
XX W09420617-A2.
XX
PD 15-SEP-1994.
XX
PF 08-MAR-1994; 94WO-US002447.
XX
PR 08-MAR-1993; 93US-00028031.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
XX Elliott KJ, Ellis SB, Harpold MM;
XX
DR WPI; 1994-303024/37.
XX N-PSDB; AAV12197.
XX
XX Human neuronal nicotinic acetylcholine receptor subunits and DNA - also
XX transformed cells useful for screening cpds. which modulate activity of
XX the receptor.
XX
XX Claim 7; Page 80-81; 99pp; English.
XX
XX The present sequence represents a human neuronal nicotinic acetylcholine
XX receptor (NACHR) subunit. The cells expressing the alpha and/or beta
XX NACHR subunits may be used in a method of screening compounds to identify
XX any which modulate the activity of human neuronal NACHR. Subunit specific
XX antibodies may be used to monitor the distribution and expression of
XX of various subunits in normal vs diseased brain tissues. Testing of
XX single receptor subunits or specific receptor subunit combinations with a
XX variety of potential agonists or antagonists provides information with
XX respect to the function and activity of the individual subunits and
XX should lead to the identification and design of compounds that are
XX capable of very specific interaction with one or more receptor subtypes.
XX The resulting drugs should exhibit fewer unwanted side effects than drugs
XX identified e.g. screening with cells that express a variety of subtypes
XX Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60

QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RFDATEHTNVLVNSGHCQYLPPIGPKSCYIDVRWPFPPDVQHCXKFKGWSYGGWSLDL 180
DB 121 RFDATEHTNVLVNSGHCQYLPPIGPKSCYIDVRWPFPPDVQHCXKFKGWSYGGWSLDL 180

QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECKEYPDVTFTVTRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECKEYPDVTFTVTRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300

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Db      241  CVLISALALLVFLPADSGEKISLIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
QY      301  MIIVGLSVVTVIVLYQHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db      301  MIIVGLSVVTVIVLYQHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY      361  QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db      361  QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY      421  LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
AAW09025
ID  AAW09025 standard; protein; 502 AA.
XX
AC  AAW09025;
DT
DT  09-APR-1997 (first entry)
XX
DE  Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
XX
KW  Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
KW  ligand-gated receptor.
XX
OS  Homo sapiens.
XX
PN  WO9641876-A1.
XX
PD  27-DEC-1996.
XX
PF  07-JUN-1996; 96WO-US009775.
XX
PR  07-JUN-1995; 95US-00484722.
XX
PA  (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI  Elliott KJ, Harpold MM;
XX
DR  WPI; 1997-065463/06.
XX
DR  N-PSDB; AAT48239.
XX
PT  Nucleic acids encoding nicotinic acetylcholine receptor sub-units - used
PT  in screening to determine the effect of drugs on the receptor.
XX
PS  Disclosure; Page 73-74; 108pp; English.
XX
CC  The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
CC  acetylcholine receptor (nAChR) can be expressed in transformed host cells
CC  carrying alpha-7 subunit DNA (see also AAT48239). Host cells, esp.
CC  mammalian cells or amphibian oocytes, expressing the recombinant alpha-7
CC  subunit, opt. in combination with other recombinant alpha and/or beta
CC  subunits (see also AAW09018-24, AAW09026-27), can be used to examine the
CC  function of human AChR and to identify cpds. that modulate its activity
XX
SQ  Sequence 502 AA;

Query Match          99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  MRCSPGGVWLAAASLLHVSQGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
Db      1  MRCSPGGVWLAAASLLHVSQGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
QY      61  QIMDVDEKNQVLTITNWLQMSWTDHYLQWNVSEYFGVKTVPDQGIWKPDILLYNSADE 120

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```

Db      61  QIMDVDEKNQVLTITNWLQMSWTDHYLQWNVSEYFGVKTVPDQGIWKPDILLYNSADE 120
QY      121  RFDATFHTNVLVNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
Db      121  RFDATFHTNVLVNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
QY      181  QMQEADISGIYPNGSMDLVGIPGKSERFYECKEPPYDVTFTVTRRTLYYGLNLLIP 240
Db      181  QMQEADISGIYPNGSMDLVGIPGKSERFYECKEPPYDVTFTVTRRTLYYGLNLLIP 240
QY      241  CVLISALALLVFLPADSGEKISLIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
Db      241  CVLISALALLVFLPADSGEKISLIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
QY      301  MIIVGLSVVTVIVLYQHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db      301  MIIVGLSVVTVIVLYQHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY      361  QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db      361  QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY      421  LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4
AAB24088
ID  AAB24088 standard; protein; 502 AA.
XX
AC  AAB24088;
DT
DT  29-JAN-2001 (first entry)
XX
DE  Human PRO2145 protein sequence SEQ ID NO:77.
XX
KW  Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW  proliferation; tumorigenesis; identification; cancer; cytostatic;
KW  neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW  immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW  neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW  hypothalamic disorder; glandular disorder; macrophagal disorder;
KW  epithelial disorder; stromal disorder; blastocoeleic disorder;
KW  inflammatory disorder; immunologic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200053755-A2.
XX
PD  14-SEP-2000.
XX
PF  06-JAN-2000; 2000WO-US000376.
XX
PR  08-MAR-1999; 99WO-US005028.
PR  02-JUN-1999; 99WO-US012252.
PR  23-JUN-1999; 99US-0141037F.
PR  07-JUL-1999; 99US-0143048P.
PR  26-JUL-1999; 99US-0145698P.
PR  30-NOV-1999; 99WO-US028313.
PR  20-DEC-1999; 99WO-US030911.
PR  05-JAN-2000; 2000WO-US000219.
XX
(GETH ) GENENTECH INC.
PA
XX  Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI  Watanabe CK, Wood WI;
XX

```

DR	WPI; 2000-572270/53.	
XX	N-PSDB; AAC58395.	
PT	Thirty PRO polynucleotides encoding PRO polypeptides, useful in the	
PT	treatment, diagnosis and prevention of cancer.	
XX		
PS	Claim 61; Fig 58; 286pp; English.	
XX		
CC	The present invention describes an isolated antibody that binds to one of	
CC	the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,	
CC	PRO1717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,	
CC	PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,	
CC	PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR	
CC	PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The	
CC	PRO polypeptides and nucleotides are useful in the treatment, diagnosis	
CC	and prevention of cancer. The antibodies and other anti-tumour compounds	
CC	may be used to treat various conditions, including those characterised by	
CC	overexpression and/or activation of the amplified PRO genes. Exemplary	
CC	conditions or disorders to be treated with such antibodies and other	
CC	compounds include benign or malignant tumours (e.g., renal, liver,	
CC	kidney, bladder, breast, gastric, ovarian, colorectal, prostate,	
CC	pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,	
CC	glioblastomas, and various head and neck tumours), leukaemias and	
CC	lymphoid malignancies, other disorders such as neuronal, glial,	
CC	astrocytal, hypothalamic and other glandular, macrophagal, epithelial,	
CC	stromal and blastocoealic disorders, and inflammatory, angiogenic and	
CC	immunologic disorders. AAC58242 to AAC58366 represent PCR primers and	
CC	hybridisation probes used in the isolation of the human PRO sequences.	
CC	AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO	
CC	polynucleotide and protein sequences given in the exemplification of the	
CC	present invention	
XX		
SQ	Sequence 502 AA;	
Query Match		99.8%; Score 2698; DB 3; Length 502;
Best Local Similarity		99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative		0; Mismatches 1; Indels 0; Gaps 0;
QY	1 MRCSPGVWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVDNSOPLTVYFSLSL 60	
Db	1 MRCSPGVWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVDNSOPLTVYFSLSL 60	
QY	61 QIMDVDEKNQVLTNINLQMSWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLNSADE 120	
Db	61 QIMDVDEKNQVLTNINLQMSWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLNSADE 120	
QY	121 RFDATFHTNVLNNSGHCQYLPFGIPKSSCYIDVRWFPDPVOHCKLKFGSWSYGGWSLDL 180	
Db	121 RFDATFHTNVLNNSGHCQYLPFGIPKSSCYIDVRWFPDPVOHCKLKFGSWSYGGWSLDL 180	
QY	181 QMOEADISGYIPNGEWDLVGIPKGSERFEYCKEPYDPVTFTVMRRRTLYYGLNLLIP 240	
Db	181 QMOEADISGYIPNGEWDLVGIPKGSERFEYCKEPYDPVTFTVMRRRTLYYGLNLLIP 240	
QY	241 CVLISALALLVLLPADSCEKISLGTITVLLSTTFMLLVAETMPATSDSVPLIAQYFAST 300	
Db	241 CVLISALALLVLLPADSCEKISLGTITVLLSTTFMLLVAETMPATSDSVPLIAQYFAST 300	
QY	301 MIIVGLSVVVTVIQLYHHHDPGGKMPKWTRVILLNWCWFLRMKRPGEEDKVRPACQHK 360	
Db	301 MIIVGLSVVVTVIQLYHHHDPGGKMPKWTRVILLNWCWFLRMKRPGEEDKVRPACQHK 360	
QY	361 QRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTPDPSGVCCGMACTHDEHL 420	
Db	361 QRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTPDPSGVCCGMACTHDEHL 420	
QY	421 LHGGQPPGDPDLAKLLEEVRIANFRQDSEAVCSWKFAACVVDRLCLMAFSVF 480	
Db	421 LHGGQPPGDPDLAKLLEEVRIANFRQDSEAVCSWKFAACVVDRLCLMAFSVF 480	
QY	481 ICTIGILMSAPNFVEAVSKDFA 502	
Db	481 ICTIGILMSAPNFVEAVSKDFA 502	

RESULT 5	
AAB82690	
ID	AAB82690 standard; protein; 502 AA.
XX	
AC	AAB82690;
XX	
DT	15-OCT-2001 (first entry)
XX	
DE	Nicotinic acetylcholine receptor alpha7.
XX	
KW	Nicotinic acetylcholine receptor; nAChR; human;
KW	acetylcholine binding protein; AChBP; mollusc; ligand-binding protein;
KW	ligand-gated ion channel; crystal; drug design; protein co-ordinate data;
KW	schizophrenia; Alzheimer's disease; nicotine addiction;
KW	Tourette's syndrome; therapy; nootropic; neuroprotective.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	108..115
FT	/note= "conserved ligand-binding region, residues Trp108
FT	and Tyr115 are essential"
FT	171..173
FT	/note= "conserved ligand-binding region, residues Trp171
FT	and Tyr173 are essential"
FT	210..217
FT	/note= "conserved ligand-binding region, residues Tyr210,
FT	Cys212, Cys213 and Tyr217 are essential"
XX	
PN	WO200158951-A2.
XX	
PD	16-AUG-2001.
XX	
XX	09-FEB-2001; 2001WO-EP001457.
XX	
PR	10-FEB-2000; 2000EP-00200443.
PR	31-OCT-2000; 2000EP-00203810.
XX	
PA	(TEWE-) STICHTING TECH WETENSCHAPPEN.
XX	
PI	Smit AB, Sixma TK;
XX	
DR	WPI; 2001-497071/54.
XX	
PT	Water-soluble ligand-binding proteins derived from molluscs and analogs
PT	of ligand-gated ion channels, useful in drug screening assay, where the
PT	drugs identified can be used in the treatment of Alzheimer's disease or
PT	schizophrenia.
XX	
PS	Disclosure; Page 252-254; 260pp; English.
XX	
CC	The present sequence is that of the alpha subunit of human nicotinic
CC	acetylcholine receptor (nAChR). The sequence includes regions that are
CC	conserved throughout the various nAChR alpha subunits and which are
CC	essential for ligand binding. The invention relates to water-soluble
CC	ligand-binding proteins derived from molluscs, especially acetylcholine-
CC	binding proteins (AChBP) and analogues of ligand-gated ion channels,
CC	their crystals, and their use for screening ligands of ligand-gated ion
CC	channels. The water-soluble ligand-binding proteins are capable of
CC	forming multimers and are amenable to crystallization. The crystal
CC	structure of AChBP is provided, and can be used to generate 3D models of
CC	the extracellular ligand-binding domain of ligand-gated ion channels and
CC	thus for screening of drugs that act on these ion channels. Chimeric
CC	proteins are provided that are capable of binding a ligand of a ligand-
CC	gated receptor, and comprise at least the amino acids of the AChBP
CC	determining solubility of the AChBP, in the same positions as in the
CC	AChBP, and also comprising amino acids determining binding to the ligand.
CC	In the chimeric proteins, at least the essential amino acids of at least
CC	1 of the conserved regions of an nAChR have been substituted for the
CC	corresponding amino acids, and preferably entire stretches have been
CC	substituted. New drugs can be developed that selectively intervene in

CC neuronal signalling pathways, especially where the ligand-gated ion
 CC channel is the nAChR, and the related disorder is Tourette's syndrome,
 CC Alzheimer's disease, addiction to nicotine or schizophrenia
 XX
 SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 4; Length 502;
 Best Local Similarity 99.8%; Pred. No. 2.2e-262;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWMLAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
 DB 1 MRCSPGGVWMLAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
 QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
 QY 121 RPDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSGWSL 180
 DB 121 RPDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSGWSL 180
 QY 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTWRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTWRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360
 DB 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
 AAB50012
 ID AAB50012 standard; protein; 502 AA.
 XX
 AC AAB50012;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Wild-type human alpha7 ligand gated ion channel.
 XX
 KW Human; alpha7 nicotinic acetylcholine gated ion channel;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
 XX
 OS Homo sapiens.
 XX
 PN WO200073431-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 25-MAY-2000; 2000WO-US011862.
 XX
 PR 27-MAY-1999; 99US-0136174P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Groppi VE, Wolfe ML, Berkenpas MB;

XX WPI: 2001-061524/07.
 DR N-PSDB; AAC90380.
 XX
 PT Special cell culture medium for treating cells and for inducing mammalian
 PT cell lines to conduct calcium ions, comprising specified concentrations
 of ions of sodium, calcium and potassium at specified pH.
 XX
 PS Disclosure; Page 61-63; 77pp; English.
 XX
 CC The present sequence is wild-type human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the cells
 XX
 SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 4; Length 502;
 Best Local Similarity 99.8%; Pred. No. 2.2e-262;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWMLAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
 DB 1 MRCSPGGVWMLAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
 QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
 QY 121 RPDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSGWSL 180
 DB 121 RPDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSGWSL 180
 QY 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTWRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTWRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360
 DB 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 7
 ABG70492
 ID ABG70492 standard; protein; 502 AA.
 XX
 AC ABG70492;
 XX
 DT 06-DEC-2002 (first entry)
 XX
 DE Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
 XX
 KW Human; neuronal nicotinic acetylcholine receptor; nAChR; receptor;
 KW ion flux; alpha 7 subunit.
 XX

OS Homo sapiens.
PN US6440681-B1.
XX 27-AUG-2002.
PD 07-JUN-1995; 95US-00487596.
XX 03-APR-1990; 90US-00504455.
PR 20-NOV-1992; 92US-00938154.
PR 08-MAR-1993; 93US-00028031.
XX 08-NOV-1993; 93US-00149503.
XX (MERI) MERCK & CO INC.
PA Elliott KJ, Ellis SB, Harpold MM;
XX WPI; 2002-711528/77.
XX N-PSDB; ABS54875.
DR Identifying antagonists or agonists of human neuronal nicotinic
XX acetylcholine receptors, by contacting recombinant cells with test
PT compound, and measuring ion flux of cells or binding of compound to
PT nNACHR.
XX Claim 101; Col 59-64; 56pp; English.
XX The invention relates to a method for identifying compounds that are
CC antagonists or agonists of human neuronal nicotinic acetylcholine
CC receptors (nNACHR), by contacting recombinant cells with a test compound
CC and measuring ion flux, the electrophysiological response of the cells or
CC binding of the test compound to the nNACHR. The recombinant cells are
CC produced by transfection with a nucleic acid encoding at least one human
CC nNACHR (alpha or beta) subunit, such that the cells express an nNACHR
CC comprising one human subunit encoded by the transfected nucleic acid.
CC This sequence represents the alpha 7 subunit of the human nNACHR
XX polypeptide
XX
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 5; Length 502;
Best Local Similarity 99.8%; Pred. NO. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALAAALLHVSLQGEFORKLYKELVKNYNPLERPVPANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAALAAALLHVSLQGEFORKLYKELVKNYNPLERPVPANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLNNSGHCQYLPPIGPKSCYIDVRFPDVQHCCLKFGSWYGGWSLDL 180
DB 121 RFDATFHTNVLNNSGHCQYLPPIGPKSCYIDVRFPDVQHCCLKFGSWYGGWSLDL 180
QY 181 OMQEADISGVINGEWDLVGIPKRSERFYECKEYDPDVTFTVTRRTLYYGNLLIP 240
DB 181 OMQEADISGVINGEWDLVGIPKRSERFYECKEYDPDVTFTVTRRTLYYGNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGTIVLLSLTTFMLLVAEIMPATSDSVPIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGTIVLLSLTTFMLLVAEIMPATSDSVPIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGQPKWTRVILLNWCWFLRMKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPGGQPKWTRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY 361 QRCRCSLASVEMSAVAPPASGNLLYIGRGLDGVHCVPTPDGCVVCGRMACSPTHDEHL 420
DB 361 QRCRCSLASVEMSAVAPPASGNLLYIGRGLDGVHCVPTPDGCVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILLEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

DB 421 LHGGQPPEGDPDLAKILLEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 8
AB882435
ID ABB82435 standard; protein; 502 AA.
XX ABB82435;
XX 22-JAN-2003 (first entry)
XX Human neuronal NACHR alpha7 subunit.
XX Human; neuronal; nicotinic acetylcholine receptor; NACHR; drug screening;
KW immunochemistry; NACHR alpha7 subunit; receptor.
XX Homo sapiens.
OS
XX WO200259266-A2.
PN 01-AUG-2002.
XX 29-OCT-2001; 2001WO-US050985.
PR 01-NOV-2000; 2000US-00703951.
XX (MERI) MERCK & CO INC.
XX Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
PI WPI; 2002-698532/75.
DR N-PSDB; ABV73248.
XX Cell comprising nucleic acids encoding human alpha and beta subunits of
PT neuronal nicotinic acetylcholine receptors, useful for in vitro screening
PT of a drug substance in a test system specific for humans.
XX Example; Page 130-131; 143pp; English.
XX The invention relates to a suitable host cell transfected with an
CC isolated nucleic acid molecule comprising a sequence of nucleotides or
CC ribonucleotides that encodes at least one alpha or beta subunit of a
CC human neuronal nicotinic acetylcholine receptor (NACHR). The compositions
CC and methods of the present invention, which provide a means to prepare
CC synthetic or recombinant receptors and receptor subunits that are
CC substantially free of contamination from many other receptor proteins,
CC are useful for observing the effect of a drug substance on a particular
CC subtype to perform in vitro screening of the drug substance in a test
CC system that is specific for humans. The antibodies can be used in
CC immunochemistry and for diagnostic and therapeutic applications. The
CC present sequence represents a human neuronal NACHR alpha7 subunit
XX
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 5; Length 502;
Best Local Similarity 99.8%; Pred. NO. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALAAALLHVSLQGEFORKLYKELVKNYNPLERPVPANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAALAAALLHVSLQGEFORKLYKELVKNYNPLERPVPANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLNNSGHCQYLPPIGPKSCYIDVRFPDVQHCCLKFGSWYGGWSLDL 180

Db 121 RPDATFHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFPDQVHCKLKFGSWYGGWSLDL 180
QY 181 QMOEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVTRRTLYYGLNLLIP 240
Db 181 QMOEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVTRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGTITVLSLTTFMLLVAEIMPATSDSVPLIAQVFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTITVLSLTTFMLLVAEIMPATSDSVPLIAQVFAST 300
QY 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDEVKVRACQHK 360
Db 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDEVKVRACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVGCRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVGCRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 9
ADA10874
ID ADA10874 standard; protein; 502 AA.
AC ADA10874;
XX
XX
DT 06-NOV-2003 (first entry)
DE Human neuronal nicotinic acetylcholine receptor alpha 7 subunit #1.
XX
XX
KW alpha 7 subunit; human; neuronal nicotinic acetylcholine receptor;
KW ligand-gated ion channel; synaptic transmission; gene therapy;
KW transgenic; receptor.
XX
XX
OS Homo sapiens.
XX
FN US6524789-B1.
XX
PD 25-FEB-2003.
XX
PF 07-JUN-1996; 96US-00660451.
XX
PR 07-JUN-1995; 95US-00484722.
XX
PA (MERI) MERCK & CO INC.
XX
PI Elliott KJ, Harpold MM;
XX
XX WPI; 2003-511917/48.
DR N-PSDB; ADA10864.
XX
XX New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human
PT neuronal nicotinic acetylcholine receptor (nAChR), useful for identifying
PT compounds that modulate human neuronal nAChR activity.
XX
XX Disclosure; Col 67-72; 63pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
CC nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human
CC neuronal nicotinic acetylcholine receptor nAChR. nAChR's form ligand-
CC gated ion channels that mediate synaptic transmissions between nerve and
CC muscle and between neurons upon interaction with the neurotransmitter
CC acetylcholine. The nucleic acid molecule is useful for identifying
CC compounds that modulate human neuronal nAChR. The present sequence
CC represents the amino acid sequence of the human neuronal nicotinic
CC acetylcholine receptor, nAChR, alpha 7 subunit #1. Note: the present

CC sequence is the sequence encoded by the nAChR alpha 7 subunit DNA
CC ADA10864.
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 7; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGCVWLAAALSHVSLQGEFQRLYKELVKNYNPLRPVANDSPLTVYFSLSL 60
Db 1 MRCSPGCVWLAAALSHVSLQGEFQRLYKELVKNYNPLRPVANDSPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNVSEYGVKTVRPDGOIKWKPDIILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNVSEYGVKTVRPDGOIKWKPDIILLYNSADE 120
QY 121 RPDATFHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFPDQVHCKLKFGSWYGGWSLDL 180
Db 121 RPDATFHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFPDQVHCKLKFGSWYGGWSLDL 180
QY 181 QMOEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVTRRTLYYGLNLLIP 240
Db 181 QMOEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVTRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGTITVLSLTTFMLLVAEIMPATSDSVPLIAQVFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTITVLSLTTFMLLVAEIMPATSDSVPLIAQVFAST 300
QY 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDEVKVRACQHK 360
Db 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDEVKVRACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVGCRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVGCRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 10
ADA47051
ID ADA47051 standard; protein; 502 AA.
XX
AC ADA47051;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein NP_000737, SEQ ID NO 12739.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; NP_000737.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
PS Example 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 7; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALAAASLLHVSLQGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAALAAASLLHVSLQGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNIWLQMSWDHYLQWNVSEYFGVKTVPDQGIWKPDILLVNSADE 120
DB 61 QIMDVDEKNQVLTNIWLQMSWDHYLQWNVSEYFGVKTVPDQGIWKPDILLVNSADE 120
QY 121 RFDATFHTNVLVNSSGHCOYLPPIFKSCYIDVRWFPDVQVCHLKFQSWSYGWSGLDL 180
DB 121 RFDATFHTNVLVNSSGHCOYLPPIFKSCYIDVRWFPDVQVCHLKFQSWSYGWSGLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERYECKEPYDPVDTVTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSERYECKEPYDPVDTVTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSTTVMLLVAEIMPATSDSVPLIAQYFAS 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSTTVMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVILLNWCWFLMKRKGEDKVRPACQHK 360
DB 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVILLNWCWFLMKRKGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420

DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
QY 421 LHGGOPPEGDDPLAKILREVRYIANRFRQDESEAVCSWKFAACVDRCLCLMAFSVFTI 480
DB 421 LHGGOPPEGDDPLAKILREVRYIANRFRQDESEAVCSWKFAACVDRCLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 11
ADES7310
ID ADE57310 standard; protein; 502 AA.
AC ADE57310;
XX
XX 29-JAN-2004 (first entry)
XX Human Protein P36544, SRQ ID NO 3171.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P36544.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX
 XX Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 7; Length 502;
 Best Local Similarity 99.8%; Pred. No. 2.2e-262;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSL 60
 DB 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120
 QY 121 RFDATFHTNVLNVSNGHCQYLPFGIPKSSCYIDVRWFPDVQHCCKLKFGSWSYGW 180
 DB 121 RFDATFHTNVLNVSNGHCQYLPFGIPKSSCYIDVRWFPDVQHCCKLKFGSWSYGW 180
 QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVWRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVWRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPCGEDKVRPACQHK 360
 DB 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPCGEDKVRPACQHK 360
 QY 361 ORRCSLASVEMSAVAPPASNGNLLYIGRGLDGHCVPTPDGSGVCGRMACSPTHDEHL 420
 DB 361 ORRCSLASVEMSAVAPPASNGNLLYIGRGLDGHCVPTPDGSGVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRCLCLMAFSVFTI 480
 DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRCLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 12

ID ADM68431
 AC ADM68431 standard; protein; 502 AA.

AC ADM68431;
 AC ADM68431;

DT 03-JUN-2004 (first entry)

XX Human nicotinic acetylcholine receptor alpha 7 subunit #2.

XX Human; neuronal nicotinic acetylcholine receptor; alpha subunit;
 KW receptor; nAChR; neuronal disorder; Alzheimer's disease.

XX Homo sapiens.

XX US2003138911-A1.

XX 24-JUL-2003.

XX 23-JAN-2003; 2003US-00349836.

XX 07-JUN-1995; 95US-00484722.

XX 07-JUN-1996; 96US-00660451.

XX

PA

(MERI) MERCK & CO INC.

PI Elliott KJ, Harpold MM;

XX WPI; 2003-851732/79.

DR N-PSDB; ADM68421.

XX

PT New nucleic acid molecule, useful for preparing a composition for
 diagnosing or treating neuronal disorders, e.g. Alzheimer's disease.

XX

PS Disclosure; Page 35-37; 57pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule comprising a
 sequence of nucleotides encoding an alpha 6 or beta 3 subunit of a human
 neuronal nicotinic acetylcholine receptor (nAChR). Also included are
 CC isolating DNA encoding a human nicotinic acetylcholine receptor subunit,
 cells (comprising a nucleic acid molecule where the cells are prokaryotic
 CC cells or eukaryotic cells and the nucleic acid is heterologous to the
 CC cells) and identifying functional neuronal nicotinic acetylcholine
 CC receptor subunits and their combinations. The nucleic acid molecule is
 CC useful for preparing a composition for diagnosing or treating neuronal
 CC disorders, e.g. Alzheimer's disease. The present sequence represents a
 CC nAChR alpha subunit. NOTE: The present sequence is encoded by ADM68421
 CC but differs from the sequence appearing as ADM68422.

XX Sequence 502 AA;
 SQ

Query Match 99.8%; Score 2698; DB 7; Length 502;

Best Local Similarity 99.8%; Pred. No. 2.2e-262;

Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSL 60

DB 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSL 60

QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120

DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIWKPDILLYNSADE 120

QY 121 RFDATFHTNVLNVSNGHCQYLPFGIPKSSCYIDVRWFPDVQHCCKLKFGSWSYGW 180

DB 121 RFDATFHTNVLNVSNGHCQYLPFGIPKSSCYIDVRWFPDVQHCCKLKFGSWSYGW 180

QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVWRRRTLYYGLNLLIP 240

DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVWRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPCGEDKVRPACQHK 360

DB 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPCGEDKVRPACQHK 360

QY 361 ORRCSLASVEMSAVAPPASNGNLLYIGRGLDGHCVPTPDGSGVCGRMACSPTHDEHL 420

DB 361 ORRCSLASVEMSAVAPPASNGNLLYIGRGLDGHCVPTPDGSGVCGRMACSPTHDEHL 420

QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRCLCLMAFSVFTI 480

DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRCLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502

DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 13

AEB90709

ID AEB90709 standard; protein; 502 AA.

XX AEB90709;

AC AEB90709;

XX 06-OCT-2005 (first entry)
 XX Human alpha 7 nAChR wild-type protein SeqID7.
 DE protein purification; acetylcholine; Nicotinic ACh; neuroprotective;
 XX gene therapy; neurodegenerative disease; mood disorder; immune disorder.
 XX Homo sapiens.
 XX US2005170360-A1.
 XX 04-AUG-2005.
 XX 30-JAN-2004; 2004US-00769085.
 XX 30-JAN-2004; 2004US-00769085.
 XX (PAPK/) PAPKE R L.
 XX (PLAC/) PLACZEK A.
 XX Papke RL, Placzek A;
 XX WPI; 2005-562714/57.
 DR N-PSDB; AEB90708.
 XX Novel isolated variant alpha 7 nicotinic acetylcholine receptor
 PT polypeptide having second transmembrane domain comprising serine residue
 PT in sixth amino acid position, useful for treating neurological
 PT conditions.
 XX Disclosure; SEQ ID NO 7; 89pp; English.
 XX This invention relates to a novel isolated variant alpha 7 nicotinic
 CC acetylcholine receptor (nAChR) polypeptide having a second transmembrane
 CC (TM2) domain comprising a serine residue in the sixth amino acid
 CC position. The invention may be useful for the development of compounds
 CC with a neuroprotective activity whilst the disclosed sequence may prove
 CC useful for gene therapy. The invention is useful for treating conditions
 CC associated with neurodegenerative processes, enzymatic function,
 CC affective disorders or immuno function. The present sequence is that of a
 CC wild-type nAChR protein which was used during the isolation of the novel
 CC variant nAChR alpha-7 receptors of the invention.
 XX Sequence 502 AA;
 SQ
 Query Match 99.8%; Score 2698; DB 9; Length 502;
 Best Local Similarity 99.8%; Pred. No. 2.2e-262;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKYNPLERPVANDSPLTVYFSLSL 60
 DB 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKYNPLERPVANDSPLTVYFSLSL 60
 QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRPDQGIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRPDQGIWKPDILLYNSADE 120
 QY 121 RPDATHTNVLVNSSGHCQYLPFGIFKSCYIDVRFPDVOHQCKLKFGSWSYGWSL 180
 DB 121 RPDATHTNVLVNSSGHCQYLPFGIFKSCYIDVRFPDVOHQCKLKFGSWSYGWSL 180
 QY 181 QMQEADISGYPNGEWDLVGIPKRSERFVECKEYPDVTFTVTRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYPNGEWDLVGIPKRSERFVECKEYPDVTFTVTRRTLYYGLNLLIP 240
 QY 241 CVLISALLVFLPADSGEKISLGTIVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALLVFLPADSGEKISLGTIVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVTVLQYHHHDPDGGKMPKWTIVILLNCAWFLMKRPGEDKVRPACQHK 360
 DB 301 MIIVGLSVVTVTVLQYHHHDPDGGKMPKWTIVILLNCAWFLMKRPGEDKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVFTPDGSGVVGCMACSPTHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVFTPDGSGVVGCMACSPTHDEHL 420
 QY 421 LHGGQPPEGDDPLAKLIEEVRYIANFRQDSEAVCSEWKEFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPEGDDPLAKLIEEVRYIANFRQDSEAVCSEWKEFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDPA 502
 DB 481 ICTIGILMSAPNFVEAVSKDPA 502
 RESULT 14
 AEC01800
 ID AEC01800 standard; protein; 515 AA.
 XX
 AC AEC01800;
 XX
 DT 20-OCT-2005 (first entry)
 XX
 DE Alpha-7 nicotinic receptor with HSV tag.
 XX
 KW Gastrointestinal-Gen.; Antiinflammatory; Antiulcer; Antipsoriatic;
 KW Neuroprotective; Antirheumatic; Antiarthritic; Hemostatic; Antidiabetic;
 KW Antiasthmatic; Antiallergic; Dermatological; Ophthalmological;
 KW Cytostatic; Anti-HIV; Virucide; Antibacterial; Tuberculostatic;
 KW Fungicide; Antiparkinsonian; Nootropic; Serotonin-Reuptake-Inhibitor;
 KW INPIONCHI; 5-HT3 receptor; chromosome 17q25.1; T cell.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2005073251-A1.
 XX
 PD 11-AUG-2005.
 XX
 PF 28-JAN-2005; 2005WO-GB000292.
 XX
 PR 28-JAN-2004; 2004GB-00001882.
 XX
 PA (INPH-) INPHARMATICA LTD.
 XX
 PI Lobley AE, Michalovich D, Stancovski I, Allen KE, Allen JM;
 PI Osypenko VN, Gurney AM;
 XX WPI; 2005-555693/56.
 DR
 XX
 PT Treating diseases associated with T cells, such as inflammatory bowel
 PT diseases, multiple sclerosis, psoriasis, arthritis, diabetes, asthma and
 PT Alzheimer's disease, by administering a 5-HT3 receptor protein or
 PT encoding nucleic acid.
 XX
 XX Example 7; Page 73; 122pp; English.
 PS
 XX This sequence represents the protein alpha-7 nicotinic receptor with HSV
 CC tag at the C terminal. Alpha-7 nicotinic receptor is homologous to
 CC INPIONCHI which is a non-selective cation channel which is predicted to
 CC contain four transmembrane domains and a signal peptide of 23 amino
 CC acids. It functions as a member of the 5-HT3 receptor group, preferably
 CC as a 5-HT3 receptor subunit. INPIONCHI is a 421 amino acid protein
 CC encoded by 9 exons located on human chromosome 17q25.1. INPIONCHI has
 CC been cloned from human thymus and it is expressed on mammalian cell
 CC surface membranes. It is closely related to a murine 5-HT3-b receptor
 CC subunit. INPIONCHI is used in the method of the invention for treating a
 CC disease associated with T cells in a patient. The method comprises
 CC administering to the patient an INPIONCHI polypeptide, or its fragment
 CC having 5-HT3 protein function or having an antigenic determinant, or
 CC their functional equivalent. This protein was subcloned for mammalian
 CC expression. The method of the invention and composition comprising
 CC INPIONCHI are useful for the diagnosis, prevention and/or treatment of
 CC diseases or conditions associated with T cells, such as inflammatory

CC bowel diseases (including Crohns' disease and ulcerative colitis).
CC multiple sclerosis, psoriasis, rheumatoid arthritis, thrombocytopenia,
CC type 1 diabetes mellitus, asthma, atopic dermatitis, atopic rhinitis,
CC Alzheimer's disease, Parkinson's disease and conjunctivitis, diseases
CC associated with T-cell proliferation such as leukemias, diseases
CC associated with T-cell depletion such as HIV infection, chemotherapy and
CC radiotherapy, and diseases where regulation of T cell activation is
CC required, such as cancers, viral infections, bacterial infections
CC (including tuberculosis) and fungal infections.
XX
SQ Sequence 515 AA;

Query Match 99.8%; Score 2698; DB 9; Length 515;
Best Local Similarity 99.8%; Pred. No. 2.3e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSGGWLAALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSGGWLAALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKQVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIPKSSCYIDVRWPPFDVQHCCLKFGSWSYGS 180
DB 121 RFDATFHTNVLVNSSGHCQYLPPIPKSSCYIDVRWPPFDVQHCCLKFGSWSYGS 180
QY 181 QMQEADISGYPNGEWDLVGIPKRSERFECCKEYPDPVDTFTVTRRTLYYGLNLLIP 240
DB 181 QMQEADISGYPNGEWDLVGIPKRSERFECCKEYPDPVDTFTVTRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAS 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVCVPTPPDSGVVCGRMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVCVPTPPDSGVVCGRMACSPTHDEHL 420
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 15

AD52166
ID AD52166 standard; protein; 502 AA.
XX
AC AD52166;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human alpha 7 mutant L270T protein SEQ ID NO:4.
XX
KW QT-6 cell; mutant; nicotinic alpha 7 acetylcholine receptor;
KW mutant nicotinic alpha 7 acetylcholine receptor; human.
XX
OS Synthetic.
OS Homo sapiens.
PN WO2003095976-A2.
XX
PD 20-NOV-2003.
XX

09-MAY-2003; 2003WO-US014553.

09-MAY-2002; 2002US-0378642P.

(MEMO-) MEMORY PHARM CORP.

Wang D, De Vivo M;

WPI; 2004-012192/01.

N-PSDB; ADE52165.

New QT-6 cell or QM-7 cell, useful in identifying an agent that modulates the activity or expression of the mutant nicotinic alpha7 acetylcholine receptor.

Example 1; SEQ ID NO 4; 48pp; English.

The present invention describes a QT-6 cell or QM-7 cell which comprises a heterologous mutant nicotinic alpha 7 acetylcholine receptor or its protein subunit or a polynucleotide encoding the heterologous mutant nicotinic alpha 7 acetylcholine receptor protein subunit or its fragment or variant. Also described: (1) a method of measuring the activity of the heterologous mutant nicotinic alpha 7 acetylcholine receptor; (2) a method of identifying an agent that activates or inhibits a mutant nicotinic alpha 7 acetylcholine receptor; (3) a method of identifying an agent that modulates the expression of the mutant nicotinic alpha 7 acetylcholine receptor; (4) a method of making QT-6 cell or QM-7 cell; (5) a method of producing a mutant nicotinic alpha 7 acetylcholine receptor protein subunit; and (8) a kit comprising the QT-6 cell or QM-7 cell. The QT-6 cell or QM-7 cell can be used in identifying an agent that modulates the activity or expression of the mutant nicotinic alpha 7 acetylcholine receptor. The present sequence represents the mutant human nicotinic alpha 7 acetylcholine receptor L270T, which is used in an example from the present invention.

Sequence 502 AA;

Query Match 99.6%; Score 2693; DB 8; Length 502;
Best Local Similarity 99.6%; Pred. No. 7.1e-262;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSGGWLAALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSGGWLAALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKQVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIPKSSCYIDVRWPPFDVQHCCLKFGSWSYGS 180
DB 121 RFDATFHTNVLVNSSGHCQYLPPIPKSSCYIDVRWPPFDVQHCCLKFGSWSYGS 180
QY 181 QMQEADISGYPNGEWDLVGIPKRSERFECCKEYPDPVDTFTVTRRTLYYGLNLLIP 240
DB 181 QMQEADISGYPNGEWDLVGIPKRSERFECCKEYPDPVDTFTVTRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAS 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVCVPTPPDSGVVCGRMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVCVPTPPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGOPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI 480

Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
| | | | | | | | | | | | | | | | | |
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

Search completed: March 28, 2006, 13:29:55
Job time : 190 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:34:59 ; Search time 168 Seconds
(without alignments)
1248.514 Million cell updates/sec

Title: US-10-749-075-2

Perfect score: 2703

Sequence: 1 MRCSPGGVWLAASLLHVS.....TIGILMSAPNFVEAVSKDPA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	502	2	US-08-771-737-2
2	2703	100.0	502	3	US-09-954-936-2
3	2703	100.0	502	4	US-10-749-075-2
4	2698	99.8	502	3	US-09-892-985-8
5	2698	99.8	502	4	US-10-740-083-2
6	2698	99.8	502	5	US-10-769-085-7
7	2693	99.6	502	4	US-10-434-364-4
8	2692	99.6	502	4	US-10-740-083-10
9	2690	99.5	502	4	US-10-352-684A-56
10	2690	99.5	502	4	US-10-789-241-8
11	2690	99.5	502	4	US-10-723-940-124
12	2690	99.5	502	5	US-10-756-149-5435
13	2688	99.4	502	4	US-10-740-083-12
14	2682	99.2	502	4	US-10-740-083-14
15	2675	99.0	502	5	US-10-769-085-11
16	2670	98.8	502	4	US-10-434-364-27
17	2547	94.2	502	5	US-10-769-085-5
18	2546	94.2	502	5	US-10-769-085-9
19	2543	94.1	502	5	US-10-769-085-20
20	2542	94.0	502	4	US-10-434-364-10
21	2536	93.8	499	5	US-10-769-085-13
22	2522.5	93.3	531	4	US-10-703-953-1
23	2429	89.9	502	5	US-10-769-085-15
24	2073.5	76.7	509	5	US-10-769-085-17
25	2022	74.8	446	4	US-10-349-836-12
26	1474.5	54.6	470	4	US-10-740-083-6
27	1344	49.7	246	5	US-10-938-370-9

28 1254.5 46.4 501 3 US-09-303-232-6 Sequence 6, Appli
29 1242 45.9 496 3 US-09-303-232-4 Sequence 4, Appli
30 1165 43.1 217 4 US-10-703-953-4 Sequence 4, Appli
31 1155.5 42.7 770 3 US-09-303-232-2 Sequence 2, Appli
32 1107.5 41.0 498 4 US-10-369-493-6415 Sequence 6415, Ap
33 1089.5 40.3 560 4 US-10-369-493-5169 Sequence 5169, Ap
34 1088 40.3 554 4 US-10-203-968-12 Sequence 12, Appli
35 1088 40.3 554 5 US-10-486-702-3 Sequence 3, Appli
36 998 36.9 461 4 US-10-369-493-5084 Sequence 5084, Ap
37 959 35.5 622 3 US-09-941-179A-11 Sequence 11, Appli
38 954 35.3 311 6 US-11-097-143-17841 Sequence 17841, A
39 945 35.0 529 4 US-10-349-836-2 Sequence 2, Appli
40 945 35.0 529 4 US-10-415-014-702 Sequence 702, App
41 945 35.0 529 4 US-10-415-014-704 Sequence 704, App
42 945 35.0 529 4 US-10-415-014-705 Sequence 705, App
43 945 35.0 529 4 US-10-757-262-86 Sequence 86, Appli
44 945 35.0 529 5 US-10-643-795A-112 Sequence 112, App
45 945 35.0 529 5 US-10-643-795A-121 Sequence 121, App

ALIGNMENTS

RESULT 1

US-08-771-737-2

; Sequence 2, Application US/08771737

; Publication NO. US20010006796A1

; GENERAL INFORMATION:

; APPLICANT: Briggs, Clark A.

; APPLICANT: Gopalakrishnan, Murali

; APPLICANT: McKenna, David G.

; APPLICANT: Monteggia, Lisa M.

; APPLICANT: Roch, Jean-Marc

; APPLICANT: Sullivan, James P.

; APPLICANT: Touma, Edward

; APPLICANT: Abbott Laboratories

; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE

; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF

; FILE REFERENCE: 6017.US.01

; CURRENT APPLICATION NUMBER: US/08/771,737

; CURRENT FILING DATE: 1996-12-20

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 502

; TYPE: PRT

; ORGANISM: homo sapien

US-08-771-737-2

Query Match 100.0%; Score 2703; DB 2; Length 502;

Best Local Similarity 100.0%; Pred. No. 9.8e-259; Mismatches 0; Indels 0; Gaps 0;

Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEQRKLYKELVKNYNPLERPVANDSOPLTIVYFSLSL 60
DB 1 MRCSPGGVWLAASLLHVSLOGEQRKLYKELVKNYNPLERPVANDSOPLTIVYFSLSL 60
QY 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYFGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYFGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RPDATFHTNVLVNSGHCQYLPFGIFKSCYIDVRWFPDVOHQCKLKFGSNVSGWSL 180
DB 121 RPDATFHTNVLVNSGHCQYLPFGIFKSCYIDVRWFPDVOHQCKLKFGSNVSGWSL 180
QY 181 QMOERADISGYPNGSWDLVGIQKESERYECKPYPDVTFTVTRRTTYGLNLLIP 240
DB 181 QMOERADISGYPNGSWDLVGIQKESERYECKPYPDVTFTVTRRTTYGLNLLIP 240
QY 241 CVLISALALLVFPLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFPLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVIVLYQHHHDPDGGKMPKWTTRVILLNWCANFLRMKRPGEDEVKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHHDPDGGKMPKWTTRVILLNWCANFLRMKRPGEDEVKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGOPPEGDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

US-09-954-936-2
; Sequence 2, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; PRIOR FILING DATE: 2004-09-18
; PRIOR FILING DATE: 08/771,737
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match 100.0%; Score 2703; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 9.8e-259; Mismatches 0; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFORKLYKELVKNYNPLERPVPANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLALAAASLLHVSLSQGEFORKLYKELVKNYNPLERPVPANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNNVSEYPGVKTVPDPDQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNNVSEYPGVKTVPDPDQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPDGI FKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
DB 121 RFDATFHTNVLVNSSGHCQYLPDGI FKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPPYDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPPYDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHHDPDGGKMPKWTTRVILLNWCANFLRMKRPGEDEVKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHHDPDGGKMPKWTTRVILLNWCANFLRMKRPGEDEVKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGOPPEGDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3

US-10-749-075-2
; Sequence 2, Application US/10749075
; Publication No. US20040203033A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/10/749,075
; CURRENT FILING DATE: 2003-12-30
; PRIOR APPLICATION NUMBER: US/08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-10-749-075-2

Query Match 100.0%; Score 2703; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 9.8e-259; Mismatches 0; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFORKLYKELVKNYNPLERPVPANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLALAAASLLHVSLSQGEFORKLYKELVKNYNPLERPVPANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNNVSEYPGVKTVPDPDQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNNVSEYPGVKTVPDPDQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPDGI FKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
DB 121 RFDATFHTNVLVNSSGHCQYLPDGI FKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPPYDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPPYDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHHDPDGGKMPKWTTRVILLNWCANFLRMKRPGEDEVKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHHDPDGGKMPKWTTRVILLNWCANFLRMKRPGEDEVKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPGDDDLAKILEVRYIANFRQDESEAVCEWKFPAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPGDDDLAKILEVRYIANFRQDESEAVCEWKFPAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDPA 502
DB 481 ICTIGILMSAPNFVEAVSKDPA 502

RESULT 4

US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match 99.8%; Score 2698; DB 3; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.1e-258;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTIVYFSLSL 60
DB 1 MRCSGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTIVYFSLSL 60
QY 61 QIMDVDEKKNQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRFPDGOIWKPDILLYNSADE 120
DB 61 QIMDVDEKKNQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRFPDGOIWKPDILLYNSADE 120

QY 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKSERFYECKEKPYPDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKSERFYECKEKPYPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTTPLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTTPLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPDGCKMPKWTIVILLNCWAFIRMKRPGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPDGCKMPKWTIVILLNCWAFIRMKRPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPGDDDLAKILEVRYIANFRQDESEAVCEWKFPAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPGDDDLAKILEVRYIANFRQDESEAVCEWKFPAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDPA 502
DB 481 ICTIGILMSAPNFVEAVSKDPA 502

RESULT 5

US-10-740-083-2
; Sequence 2, Application US/10740083
; Publication No. US20040132187A1
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/10/740,083
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US/09/579,250
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-740-083-2

Query Match 99.8%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.1e-258;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTIVYFSLSL 60
DB 1 MRCSGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTIVYFSLSL 60
QY 61 QIMDVDEKKNQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRFPDGOIWKPDILLYNSADE 120
DB 61 QIMDVDEKKNQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRFPDGOIWKPDILLYNSADE 120
QY 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKSERFYECKEKPYPDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKSERFYECKEKPYPDVTFTVMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLSLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLSLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPGEDKVRPACQHK 360
QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
US-10-769-085-7
; Sequence 7, Application US/10769085
; Publication No. US20050170360A1
; GENERAL INFORMATION:
; APPLICANT: Papke, Roger
; APPLICANT: Placzek, Andon
; TITLE OF INVENTION: Variant Neuronal Nicotinic Alpha-7 Receptor and Methods of Use
; FILE REFERENCE: UF-408
; CURRENT APPLICATION NUMBER: US/10/769,085
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (262)..(281)
; OTHER INFORMATION: TM2 domain
US-10-769-085-7

Query Match 99.8%; Score 2698; DB 5; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.1e-258;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFFPDVQHKLKFGSWSYGGWSL 180
Db 121 RFDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFFPDVQHKLKFGSWSYGGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLSLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLSLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPGEDKVRPACQHK 360
QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480

Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPGEDKVRPACQHK 360
QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 7
US-10-434-364-4
; Sequence 4, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; TITLE OF INVENTION: THE TRANSFECTED CELLS
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-434-364-4

Query Match 99.6%; Score 2693; DB 4; Length 502;
Best Local Similarity 99.6%; Pred. No. 9.7e-258;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFFPDVQHKLKFGSWSYGGWSL 180
Db 121 RFDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFFPDVQHKLKFGSWSYGGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLSLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLSLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKPGEDKVRPACQHK 360
QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480

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QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 8
US-10-740-083-10
; Sequence 10, Application US/10740083
; Publication No. US20040132187A1
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Mark L.
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/10740,083
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US/09/579,250
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-740-083-10

Query Match 99.6%; Score 2692; DB 4; Length 502;
Best Local Similarity 99.6%; Pred. No. 1.2e-257;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAAASLLHVSLOGEFQKLYKELVKNNPLERPANDSQPLTVYFSL 60
Db 1 MRCSGGVWLAAASLLHVSLOGEFQKLYKELVKNNPLERPANDSQPLTVYFSL 60

QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNSYRGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNSYRGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RPDATFHTNVLVNSSGHCQYLPPIGIFKSSCYIDVRWFPDQVQCKLKFGSWSYGGWSL 180
Db 121 RPDATFHTNVLVNSSGHCQYLPPIGIFKSSCYIDVRWFPDQVQCKLKFGSWSYGGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVWRRRLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVWRRRLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360
Db 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360

QY 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
Db 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 9
US-10-352-684A-56
; Sequence 56, Application US/10352684A
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; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroli, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019PINOMNIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-352-684A-56
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Query Match 99.5%; Score 2690; DB 4; Length 502;
Best Local Similarity 99.4%; Pred. No. 1.9e-257;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAAASLLHVSLOGEFQKLYKELVKNNPLERPANDSQPLTVYFSL 60
Db 1 MRCSGGVWLAAASLLHVSLOGEFQKLYKELVKNNPLERPANDSQPLTVYFSL 60

QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNSYRGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNSYRGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RPDATFHTNVLVNSSGHCQYLPPIGIFKSSCYIDVRWFPDQVQCKLKFGSWSYGGWSL 180
Db 121 RPDATFHTNVLVNSSGHCQYLPPIGIFKSSCYIDVRWFPDQVQCKLKFGSWSYGGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVWRRRLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVWRRRLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360
Db 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360

QY 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
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Db 361 QRRCSLASVEMSAVGGPPASNGNLLYIGFRGLDGVHCVTPDPSGVCGSMACSPTHDEHL 420
Qy 421 LHGGOPPEGDDPLAKILLEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGOPPEGDDPLAKILLEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 10
US-10-789-241-8
; Sequence 8, Application US/10789241
; Publication No. US2004018032A1
; GENERAL INFORMATION:
; APPLICANT: Powell, Douglas M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 9145, 1725, 311, 837,
; TITLE OF INVENTION: 58305, 156, 14175, 50352, 32678, 5560, 7240, 8865, 12396,
; TITLE OF INVENTION: 12397, 13644, 19938, 2077, 1735, 1786, 10220, 17822, 33945,
; TITLE OF INVENTION: 43748, 47161, 81982 OR 46777
; FILE REFERENCE: MP103-041P1RNMNMN
; CURRENT APPLICATION NUMBER: US/10789,241
; CURRENT FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,202
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/456,326
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/465,240
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/475,233
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/478,952
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/487,836
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/500,111
; PRIOR FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-241-8

Query Match 99.5%; Score 2690; DB 4; Length 502;
Best Local Similarity 99.4%; Pred. No. 1.9e-257;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWLALAAALLHVSLLQGEFQRLKYKELVKNNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGGVWLGLAASLLHVSLLQGEFQRLKYKELVKNNPLERPVANDSQPLTVYFSLSL 60
Qy 61 QIMDVDEKNQVLTNNIWLQMSWDHYLQWNVSEYPGVKTVPDQGIWKPDIILYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWDHYLQWNVSEYPGVKTVPDQGIWKPDIILYNSADE 120
Qy 121 RFDAFHTNNLVNSSGHCCQYLPPIFKSSCYIDVRWFFPDVQHCKLKFGSMYSGWSL 180
Db 121 RFDAFHTNNLVNSSGHCCQYLPPIFKSSCYIDVRWFFPDVQHCKLKFGSMYSGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 QIMDVDEKNQVLTNNIWLQMSWDHYLQWNVSEYPGVKTVPDQGIWKPDIILYNSADE 120
Qy 121 RFDAFHTNNLVNSSGHCCQYLPPIFKSSCYIDVRWFFPDVQHCKLKFGSMYSGWSL 180
Db 121 RFDAFHTNNLVNSSGHCCQYLPPIFKSSCYIDVRWFFPDVQHCKLKFGSMYSGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVIQLQYHHDDPDGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360

Db 301 MIIVGLSVVTVIQLQYHHDDPDGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPDPSGVCGSMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPDPSGVCGSMACSPTHDEHL 420
Qy 421 LHGGOPPEGDDPLAKILLEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGOPPEGDDPLAKILLEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 11
US-10-723-940-124
; Sequence 124, Application US/10723940
; Publication No. US20040185468A1
; GENERAL INFORMATION:
; APPLICANT: Leonard, Sherry
; APPLICANT: Freeman, Robert
; TITLE OF INVENTION: Promoter Variants in the Alpha-7 Nicotinic Acetylcholine Receptor
; TITLE OF INVENTION: Gene
; FILE REFERENCE: VARD-07989
; CURRENT APPLICATION NUMBER: US/10723,940
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 08/956,518
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-940-124

Query Match 99.5%; Score 2690; DB 4; Length 502;
Best Local Similarity 99.4%; Pred. No. 1.9e-257;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWLALAAALLHVSLLQGEFQRLKYKELVKNNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGGVWLGLAASLLHVSLLQGEFQRLKYKELVKNNPLERPVANDSQPLTVYFSLSL 60
Qy 61 QIMDVDEKNQVLTNNIWLQMSWDHYLQWNVSEYPGVKTVPDQGIWKPDIILYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWDHYLQWNVSEYPGVKTVPDQGIWKPDIILYNSADE 120
Qy 121 RFDAFHTNNLVNSSGHCCQYLPPIFKSSCYIDVRWFFPDVQHCKLKFGSMYSGWSL 180
Db 121 RFDAFHTNNLVNSSGHCCQYLPPIFKSSCYIDVRWFFPDVQHCKLKFGSMYSGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVIQLQYHHDDPDGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360
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Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPDPSGVCGSMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPDPSGVCGSMACSPTHDEHL 420
Qy 421 LHGGOPPEGDDPLAKILLEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGOPPEGDDPLAKILLEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
|||||
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 12

US-10-756-149-5435

; Sequence 5435, Application US/10756149

; Publication No. US20050181375A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND

; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

; FILE REFERENCE: file

; CURRENT APPLICATION NUMBER: US/10/756,149

; CURRENT FILING DATE: 2004-01-12

; NUMBER OF SEQ ID NOS: 5818

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5435

; LENGTH: 502

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-756-149-5435

Query Match 99.5%; Score 2690; DB 5; Length 502;

Best Local Similarity 99.4%; Pred. No. 1.9e-257;

Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFQKLYKELVKVYNPLERPVANDSPLTVYFSL 60

Db 1 MRCSPGGVWLGLAASLLHVSLSQGEFQKLYKELVKVYNPLERPVANDSPLTVYFSL 60

QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGIWKPDILLYNSADE 120

Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGIWKPDILLYNSADE 120

QY 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFPDVOHCKLKFGSWSYGWSL 180

Db 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFPDVOHCKLKFGSWSYGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240

Db 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300

Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMKRPGEDKVRPACQHK 360

Db 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMKRPGEDKVRPACQHK 360

QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDSGVVCGRMACSPTHDEHL 420

Db 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPEGDDPLAKILEEVRYIANFRCDSEAVCSEWKPFAACVVDRLCLMAFSVFTI 480

Db 421 LHGGQPPEGDDPLAKILEEVRYIANFRCDSEAVCSEWKPFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502

Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 13

US-10-740-083-12

; Sequence 12, Application US/10740083

; Publication No. US20040132187A1

; GENERAL INFORMATION:

; APPLICANT: Groppi, Vincent

; APPLICANT: Wolfe, Mark L.
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; TITLE OF INVENTION: Conductance
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/10/740,083
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US/09/579,250
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-740-083-12

Query Match 99.4%; Score 2688; DB 4; Length 502;

Best Local Similarity 99.6%; Pred. No. 3e-257;

Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFQKLYKELVKVYNPLERPVANDSPLTVYFSL 60

Db 1 MRCSPGGVWLALAAASLLHVSLSQGEFQKLYKELVKVYNPLERPVANDSPLTVYFSL 60

QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGIWKPDILLYNSADE 120

Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGIWKPDILLYNSADE 120

QY 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFPDVOHCKLKFGSWSYGWSL 180

Db 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFPDVOHCKLKFGSWSYGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240

Db 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300

Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMKRPGEDKVRPACQHK 360

Db 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMKRPGEDKVRPACQHK 360

QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDSGVVCGRMACSPTHDEHL 420

Db 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPEGDDPLAKILEEVRYIANFRCDSEAVCSEWKPFAACVVDRLCLMAFSVFTI 480

Db 421 LHGGQPPEGDDPLAKILEEVRYIANFRCDSEAVCSEWKPFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502

Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 14

US-10-740-083-14

; Sequence 14, Application US/10740083

; Publication No. US20040132187A1

; GENERAL INFORMATION:

; APPLICANT: Groppi, Vincent

; APPLICANT: Wolfe, Mark L.

; APPLICANT: Berkenpas, Mitchell B

; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel

; TITLE OF INVENTION: Conductance

; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists

; CURRENT APPLICATION NUMBER: US/10/740,083

; CURRENT FILING DATE: 2003-12-18

; PRIOR APPLICATION NUMBER: US/09/579,250

; PRIOR FILING DATE: 2000-05-25

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; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-740-083-14

Query Match
Best Local Similarity 99.2%; Score 2682; DB 4; Length 502;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLALAAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
Db 121 RFDATFHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
QY 121 RFDATFHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
Db 121 RFDATFHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVVTVIQLQYHHDDPGGKMPKWTTRVILLNCAWFLMRKRGEDKVRPACQHK 360
Db 301 MIIVGLSVVVTVIQLQYHHDDPGGKMPKWTTRVILLNCAWFLMRKRGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
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RESULT 15
US-10-769-085-11
; Sequence 11, Application US/10769085
; Publication No. US20050170360A1
; GENERAL INFORMATION:
; APPLICANT: Papke, Roger
; TITLE OF INVENTION: Variant Neuronal Nicotinic Alpha-7 Receptor and Methods of Use
; FILE REFERENCE: UF-408
; CURRENT APPLICATION NUMBER: US/10/769,085
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Macaca mulatta
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (262)..(281)
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; OTHER INFORMATION:
US-10-769-085-11

Query Match
Best Local Similarity 99.0%; Score 2675; DB 5; Length 502;
Matches 496; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLALAAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
Db 121 RFDATFHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVVTVIQLQYHHDDPGGKMPKWTTRVILLNCAWFLMRKRGEDKVRPACQHK 360
Db 301 MIIVGLSVVVTVIQLQYHHDDPGGKMPKWTTRVILLNCAWFLMRKRGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

Search completed: March 28, 2006, 13:38:29
Job time : 169 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:35:49 ; Search time 25 Seconds
(without alignments)
592.247 Million cell updates/sec

Title: US-10-749-075-2
Perfect score: 2703
Sequence: 1 MRCSPGGWIALAASLLHVS.....TIGILMSAPNFVEAVSKDPA 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB_PUB.pep:*
2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB_PUB.pep:*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB_PUB.pep:*
4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB_PUB.pep:*
5: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB_PUB.pep:*
6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB_PUB.pep:*
7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB_PUB.pep:*
8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2698	99.8	502	7	US-11-122-144-12
2	945	35.0	529	7	US-11-122-144-2
3	916	33.9	627	7	US-11-037-829A-1
4	887	32.8	627	7	US-11-122-144-6
5	884	32.7	498	7	US-11-037-829A-3
6	884	32.7	498	7	US-11-122-144-18
7	882	32.6	504	7	US-11-122-144-4
8	867.5	32.1	494	7	US-11-122-144-10
9	861	31.9	502	7	US-11-122-144-14
10	850.5	31.5	485	7	US-11-037-829A-11
11	849	31.4	502	7	US-11-037-829A-2
12	832.5	30.8	491	7	US-11-037-829A-9
13	811.5	30.0	495	7	US-11-037-829A-7
14	772	28.6	458	7	US-11-122-144-16
15	770.5	28.5	468	7	US-11-122-144-8
16	571.5	21.1	478	7	US-11-037-829A-4
17	555.5	20.6	483	7	US-11-037-829A-5
18	232	8.6	485	6	US-10-204-029-7
19	221.5	8.2	475	7	US-11-241-631-16
20	221.5	8.2	487	7	US-11-241-631-14
21	216	8.0	506	7	US-11-241-631-15
22	203	7.5	473	7	US-11-169-041-229
23	195	7.2	497	7	US-11-037-829A-15
24	193	7.1	474	7	US-11-037-829A-13
25	187.5	6.9	422	6	US-10-204-029-4

26	187.5	6.9	426	6	US-10-204-029-2	Sequence 2, Appli
27	187	6.9	487	7	US-11-241-631-13	Sequence 13, Appl
28	184.5	6.8	465	7	US-11-037-829A-14	Sequence 14, Appl
29	179.5	6.6	481	6	US-10-512-376-5	Sequence 5, Appli
30	177	6.5	467	6	US-10-512-376-3	Sequence 3, Appli
31	177	6.5	496	6	US-10-512-376-2	Sequence 2, Appli
32	171.5	6.3	345	7	US-11-188-353-10	Sequence 10, Appl
33	171.5	6.3	392	7	US-11-188-353-4	Sequence 4, Appli
34	171.5	6.3	420	7	US-11-188-353-8	Sequence 8, Appli
35	171.5	6.3	459	6	US-10-512-376-6	Sequence 6, Appli
36	171.5	6.3	467	7	US-11-188-353-2	Sequence 2, Appli
37	162	6.0	448	7	US-11-241-631-17	Sequence 17, Appl
38	158	5.8	492	7	US-11-037-829A-12	Sequence 12, Appl
39	112	4.1	226	6	US-10-512-376-8	Sequence 8, Appli
40	110	4.1	504	7	US-11-087-099-1027	Sequence 1027, Ap
41	110	4.1	518	7	US-11-087-099-6795	Sequence 6795, Ap
42	97.5	3.6	556	6	US-10-613-744-8	Sequence 8, Appli
43	96.5	3.6	266	6	US-10-884-730-334	Sequence 334, App
44	96.5	3.6	266	7	US-11-000-463-381	Sequence 381, App
45	94.5	3.5	266	6	US-10-884-730-116	Sequence 116, App

ALIGNMENTS

RESULT 1

US-11-122-144-12
; Sequence 12, Application US/11122144
; Publication No. US20050287663A1
; GENERAL INFORMATION:
; APPLICANT: Gillespie, Alison
; Claepse, Brian O.
; Chavez-Noriega, Laura Elena
; Siegel, Robert
; Elliott, Kathryn J.
; TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
; OF NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR, CELLS TRANSFORMED THEREWITH,
; AND RECOMBINANT CELL LINE EXPRESSING

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 E. Lincoln Avenue

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/122,144

FILING DATE: 04-May-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/703,951

FILING DATE: 01-Nov-2000

APPLICATION NUMBER: US 08/487,596

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: WO US94/02447

FILING DATE: 08-MAR-1994

APPLICATION NUMBER: US 08/149,503

FILING DATE: 08-NOV-1993

APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MAR-1993

APPLICATION NUMBER: US 07/938,154

FILING DATE: 30-NOV-1992

APPLICATION NUMBER: US 07/504,455

FILING DATE: 03-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Kohli, Vineet

Db 390 CHFLRLKLSYHNSVDAREVVEEDRWACAGHVPASVGTLCSHGH-----LHSG 445
QY 425 QP-----PEGD-----PDALAKILEVRYIANFRCODESEAVCSWKPAACVDRCL 472
Db 446 ASGPKABALQEGELLSPHMQKALEGVHYIADHLASEADSSVKEDWKYVAMVIDRFL 505
QY 473 MAFSVFTIICIGILMSARNFV 494
Db 506 WLFIVCFGLTIGLFL--PPFL 525

RESULT 3
US-11-037-829A-1
; Sequence 1, Application US/11037829A
; Publication No. US2005025551A1
; GENERAL INFORMATION:
; APPLICANT: Targacept, Inc
; APPLICANT: Catholic Healthcare West
; APPLICANT: Bencherif, Merouane
; APPLICANT: Lukas, Ronald J.
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
; TITLE OF INVENTION: Nicotinic Receptor Subunits
; FILE REFERENCE: T103 1520.PCT
; CURRENT APPLICATION NUMBER: US/11/037,829A
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 60/397,380
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-037-829A-1

Query Match 33.9%; Score 916; DB 7; Length 627;
Best Local Similarity 33.9%; Pred. No. 1.7e-76;
Matches 207; Conservative 88; Mismatches 177; Indels 138; Gaps 11;

QY 10 LALAAILL-----HVSLLQGEFQRKLYKELVKNVYPLERPVANDSQPLTVVFSLSLLQIMDV 65
Db 17 LLTGTLGRASSHVEFRAEAEELLKKLPNGYNKSRPVANISDVVLRFGLSIALIDV 76
QY 66 DEKQVLTNIMIQMSWTNHYLQWNVSEYGVKTVRPPGQIKWPKDILLYNSADERFDT 125
Db 77 DEKNQWMTNIVVYKQEMHDKLRWDPADYENVVTSIRIPSELIWRPDIVLYNNADGFAVT 136
QY 126 FHTNVLVNSGHCQYLPPIGFIKSSCYIDVRWFFPDVQHCKLKEGWSYGGWSLDL--QMQ 183
Db 137 HLTAKHLFHDGRVQWTPPAIYKSSCIDVTFPPDQNCMTKFGSWTYDKAKIDLYNMHS 196
QY 184 EADISGVIPNGEVDLVCIPGKRSERFECCKEYPDPVTFVTWRRRTLYVGLMLLIPCVL 243
Db 197 RVQDLDFWESGEWIVDAVGTNYRKYECACAEIYDITVAFVIRRLPLFTINLIIPCLL 256
QY 244 ISALALLVFLPADSGEKISLGTIVLLSLTFTMLLVAEIMPATDSVPLIAQYFASMTII 303
Db 257 ISCLTVLVFVLPSECKEITLCSIVLLSLTVFLLLITTEIIPSTSLVPLIGYLLFTMIF 316
QY 304 VGLSVVTVTVLQYHHHDPDGGQMPKWTVRVILLNWCANFLMKRPGEDKVRPACQHKQR 363
Db 317 VTLISVITVFLNVHRSRPTMTPTWVRVFLDIVPRLLMKRP--SVYKQNC-----R 369
QY 364 CSLASVEMSAVAP-----PPASNG----- 382
Db 370 RLIESHMKWASAPRFWPEPEGEPPATSGTSLHPPSPFCVPLDVAPGPKSPKSPDQL 429
QY 383 -----NLLYIGFRG--LDG----- 394
Db 430 PPQPLEAEKASPHSPGCRPSHGTAQPLAKARSLSVQHMSSPGEAVEGGVRCRSRSI 489
QY 395 VHCVPPTDS-----GVVCGRMACSPTHDEHLLGGQP-----PEG----- 429

Db 490 QYCVPRDDAEPADQQAAGALASRNTHSAELPPQPSCKCTCKEPPSVSPSATVKTR 549
QY 430 -----DPDLAKILEVRYIANFRCODESEAVCSWKPAACVDRCLMAFSVP 478
Db 550 STKAPPPHPLSPALTRAVEGVQYIADHLKABDTDFSVKEDWKYVAMVIDRFLMFIIV 609
QY 479 TIICTIGILM 488
Db 610 CLIGTVGLFL 619

RESULT 4
US-11-122-144-6
; Sequence 6, Application US/11122144
; Publication No. US20050287663A1
; GENERAL INFORMATION:
; APPLICANT: Gillespie, Alison
; Claeps, Brian O.
; Chavez-Noriega, Laura Elena
; Siegel, Robert
; Elliott, Kathryn J.
; TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
; OF NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR. CELLS TRANSFORMED THEREWITH,
; AND RECOMBINANT CELL LINE EXPRESSING
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/122,144
; FILING DATE: 04-May-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/703,951
; FILING DATE: 01-Nov-2000
; APPLICATION NUMBER: US 08/487,596
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohli, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: SD99511A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3889
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-11-122-144-6

Query Match		32.8%; Score 887; DB 7; Length 627;
Best Local Similarity		33.4%; Pred. No. 8.2e-74;
Matches		204; Conservative 87; Mismatches 181; Indels 138; Gaps 11;
QY	10 LALAASLL-----HVSIGQEFQKLYKELVKNYNPLRPVANDSQPTVTVPSLSLQIMDV	65
DB	17 LLTGTLGRASSHIVETRAHAERLLKKLFSGYNKSRPVANISDVVLVRFGLSLAQLIDV	76
QY	66 DEKNQVLTNNIQLQMSWTQHYLQWVSEYGVKTVRFPDQIQWKPDIILYNASDERFDAT	125
DB	77 DEKNQMTTNNVWQKWBHDKLRWDPADYENVTISIRPSELWRPDIALYNADGDFAT	136
QY	126 FHTNVLNNSGHCQYLPPIGFKSSCYIDVVRFPFQVQHCKLFGSGWSYSGWSLIDL--QMQ	183
DB	137 HLTKAHLFDHGRVQRTPEPAIYKSSCSIDVTFPPDQNCNCTMKFGSWTYDKAKIDLWNHS	196
QY	184 EADISYIYNGEWDLVGIFGKRSERYECKEPYDPVTVTVMRRRTLYYGLNLLIPCVL	243
DB	197 RVDQLDFWESGEWLI3DAVGTYNTRKYECCEAIYDITYAYAIRRLPFLFTYTNLIIPWLL	256
QY	244 ISALALLVLLPADSGEKISLGTIVLLSLTTFMLLVAEIMPATSDSVPLIAOYFASTMI	303
DB	257 ISCLTALVFLPSECGEKITLCSVLSTVFLLLTETIIPSTSLVPLIGLYLLFTMIF	316
QY	304 VGLSVVTVIVLQYHHDPDGGKMPKWTRVILLNMCWFLRMKRPGEDKVRPACQHKQRR	363
DB	317 VTLSIAITVFLNVHRSRPTHMTPTVVRVFLDIIVPRLLMKRP--SVVKDNC-----R	369
QY	364 CSLASVEMSAVAP-----PPASNG-----	382
DB	370 RLIESMHKMASAPRFWPEGEPPATSGTQSLHPPSPFCVPLDVAEPGSPCKSPSDQL	429
QY	383 -----NLLYIGFRG--LDG-----	394
DB	430 PQOQPLEASKAPSPGRCRPHGTQAPGLAKARSLSVQHMSSPGEAVEGGVRCRSRI	489
QY	395 VHCVPPTDS-----GVVCGRMACSPTHDEHLLHGQP-----PEG-----	429
DB	490 QYCVPRDDAAPADGQAAGALASRNSHSAELPPDPQSPCKCTCKEPPSSVPSATVKTR	549
QY	430 -----DPDLAKILIEVRYIANRFRCODESEAVCSEWKFAACVVDRLCLMAFSPVF	478
DB	550 STKAPPPLPLSPALSRAGEVQVYIADHLKABEDTDFSVKEDWKYAMVIDRFLWFIIV	609
QY	479 TIICITIGILM 488	
DB	610 CLUGVGLFL 619	
RESULT 5		
US-11-037-829A-3		
; Sequence 3, Application US/11037829A		
; Publication No. US20050255551A1		
; GENERAL INFORMATION:		
; APPLICANT: Targacept, Inc		
; APPLICANT: Catholic Healthcare West		
; APPLICANT: Benchrif, Merouane		
; APPLICANT: Lukas, Ronald J.		
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric		
; FILE OF INVENTION: Nicotinic Receptor Subunits		
; FILE REFERENCE: T103 1520.PCT		
; CURRENT APPLICATION NUMBER: US/11/037,829A		
; CURRENT FILING DATE: 2005-01-18		
; PRIOR APPLICATION NUMBER: US 60/397,380		
; PRIOR FILING DATE: 2002-07-19		
; NUMBER OF SEQ ID NOS: 15		
; SOFTWARE: FastSeq for Windows Version 4.0		
; SEQ ID NO 3		
; LENGTH: 498		
; TYPE: PRT		
; ORGANISM: Homo sapien		
US-11-037-829A-3		
Query Match		32.7%; Score 884; DB 7; Length 498;
Best Local Similarity		39.0%; Pred. No. 1.1e-73;
Matches		184; Conservative 94; Mismatches 166; Indels 28; Gaps 9;
QY	26 QRKLYKELVK--NYNPLRPVANDSQPTVTVPSLSLQIMDVDEKNQVLTNNIQLQMSWT	83
DB	27 BEKLMDLLNTRVNNLIRPATSSQLISIKLQLSLAQLISVNEREQIMTTNNVLKQEW	86
QY	84 DHYLQWVSEYGVKTVRFPDQIQWKPDIILYNASDERFDATFHTNVLNNSGHCQYLP	143
DB	87 DYRLTWNSRYEGVNLIRIPAKRIWLPDIVLNNADGTIEVSVTNLIVRNSGSLWLP	146
QY	144 GIFKSSCYIDVVRFPFQVQHCKLFGSGWSYSGWSLIDL--LQMQEADISGYIPNGEWDLV	201
DB	147 AIYKSACKIEVKYFPDQNCNCTLKFRSNTYDHTEDMWLMTPTASMDDFTPSGEWDIV	206
QY	202 PKRSERFYECCKEP-YPDVTVTVMRRRTLYYGLNLLIPCVLISALALLVLLPADSGE	260
DB	207 PGRRTVN----PQDPSYVDVTVDFIIRKPLFTYTNLIIPCVLTTLLAILFYLPSDCGE	262
QY	261 KISLGTIVLLSLTTFMLLVAEIMPATSDSVPLIAOYFASTMIIVGLSVVTVIVLQYHH	320
DB	263 KMTLCISVLLALTFFLLISIKIVPPTSLDVPLIGLYLMFTWLVTFSTVSCVNLNHR	322
QY	321 PDGKMPKWTRVILLNMCWFLRMKRPGEDKVRPACQHKQRRCSLASVEMSAVAPPAS	380
DB	323 SPSTHTMAPWVKRCFLKLPFLFMKRPGPS-SPARAFPPSKSCVTKPEATATSTSPSN	381
QY	381 -NGNLLYIGFRGLDGVCHVPTPDSGVVCGRMACSPT---HDEHLLHGQPPGPDPLAKI	436
DB	382 FYGNSMYF-----VNPASAAKSPAGSTPVAIPRDFWFLASSGRFRQ---DVQEA	427
QY	437 LEEVRYIANRFRCODESEAVCSEWKFAACVVDRLCLMAFSPVTIICITIGILM	488
DB	428 LEGVSFIAQHMKNDDQSVVEDMKYVAMVVDRLFLWFMFVFCVLGTGLFL	479
RESULT 6		
US-11-122-144-18		
; Sequence 18, Application US/11122144		
; Publication No. US20050287663A1		
; GENERAL INFORMATION:		
; APPLICANT: Gillespie, Alison		
; Claeps, Brian O.		
; Chavez-Noriega, Laura Elena		
; Siegel, Robert		
; Elliott, Kathryn J.		
; TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS		
; OF NEURONAL NICOTINIC ACETYLCHOLINE		
; RECEPTOR, CELLS TRANSFORMED THEREWITH,		
; AND RECOMBINANT CELL LINE EXPRESSING		
; NUMBER OF SEQUENCES: 18		
; CORRESPONDENCE ADDRESS:		
; ADDRESSEE: Merck & Co., Inc.		
; STREET: 126 E. Lincoln Avenue		
; CITY: Rahway		
; STATE: NJ		
; COUNTRY: USA		
; ZIP: 07065-0907		
; COMPUTER READABLE FORM:		
; MEDIUM TYPE: Floppy disk		
; COMPUTER: IBM PC compatible		
; OPERATING SYSTEM: PC-DOS/MS-DOS		
; SOFTWARE: PatentIn Release #1.0, Version #1.25		
; CURRENT APPLICATION DATA:		
; APPLICATION NUMBER: US/11/122,144		
; FILING DATE: 04-May-2005		
; CLASSIFICATION: <Unknown>		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US/09/703,951		
; FILING DATE: 01-Nov-2000		
; APPLICATION NUMBER: US 08/487,596		

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/122,144
FILING DATE: 04-May-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/703,951
FILING DATE: 01-Nov-2000
APPLICATION NUMBER: US 08/487,596
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kohli, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: SD99511A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3889
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-122-144-14

Query Match 31.9%; Score 861; DB 7; Length 502;
Best Local Similarity 35.0%; Pred. No. 1.5e-71;
Matches 180; Conservative 102; Mismatches 192; Indels 40; Gaps 9;

QY 2 RCGPGGVTALAAASLLHVSLOG-EFORIKELIV--KNYNPLERPANDSOPLTIVYFSL 58
DB 4 RCFPVALLGFLRLCSGWGTDEERLVEHLDPKRYNKLIRPATNGSELVTVOLMVS 63
QY 59 LLIQIMVDENQVLTNNIQLWSWTDHYLQWNVSYPGVKTVPDGOIQWKPDILLYN 118
DB 64 LAQLISVHERBQIMTNVLMTQEWEDYRLTWKPPEFDNMKKVLPKSHIWLDPVVLYNNA 123
QY 119 DERPFATFTNLVNSSGHCVLPFGIFKSSCYIDVRWFPPDVQHCKLKFSWSYGWSL 178
DB 124 DGMYSFVSNAVSVSDGSIFMLPPIAYKSACKIEVGHPFPDQQNCTMKFPSWTYDRTEI 183
QY 179 DLQMOB--ADISGYIPNGEWDLVGIIPKRSERFYCCKEPYPDVTFVTMMRRRTLYYGLN 236
DB 184 DLVKESVASLDFTSGEWDIVALPRRENPD---STVVDIYDFIIKRKEFLTIN 240
QY 237 LLIPCVLISALALLVFLPADSGEKISLGITVLLSTTFFMLVAEIMPATSDSVPLIAQY 296
DB 241 LIIPCVLITSALIVFLPSDCGERKWTLICSVLLALTVELLSIKVIPPTSLDVLGVKY 300
QY 297 FASTMIIVGLSVTVIVLYHHDDGGKMPKFWTRVILLNWCAWFLBMKRPGEKVRPA 356
DB 301 LMFTWMVLTVTSVCVLNVHRSPTTHMAPWVKVPLEKLPALLFMQOQPHRCAROR 360
QY 357 CQHKQRCSLASVEMSAVAPPASNGNLVI-----GFRGLDGVHCVPTPD---SGVVC 407
DB 361 LRURHQREREGAGALFFREAPEGASCTCFCVNRASVQGLAGAFGAEPAVAGPGRSGEPC 420
QY 408 GRMACSPTHDEHLLHGQGPEDPOLAKILEEVRIANFRQCDESEAVCSWEKFAACV 467

Db 421 G---CG-----LRADVGVAFIADHRKSEDDQSVSDWKYVAMVI 458
QY 468 DRLCIMAFSVFTTIICTIGILMSAPNFVEAVSKDF 501
DB 459 DRLELWIFVFVFCVGTIGMFLO-PLFQNYTTTF 491

RESULT 10
US-11-037-829A-11
Sequence 11, Application US/11037829A
Publication No. US20050255551A1
GENERAL INFORMATION:
APPLICANT: Targacept, Inc
APPLICANT: Catholic Healthcare West
APPLICANT: Bencherif, Merouane
APPLICANT: Lukas, Ronald J.
TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
TITLE OF INVENTION: Nicotinic Receptor Subunits
FILE REFERENCE: T103 1520.PCT
CURRENT APPLICATION NUMBER: US/11/037,829A
CURRENT FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US 60/397,380
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 485
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human nChr beta4-mouse 5HT3 chimera
US-11-037-829A-11

Query Match 31.5%; Score 850.5; DB 7; Length 485;
Best Local Similarity 37.1%; Pred. No. 1.4e-70;
Matches 180; Conservative 87; Mismatches 151; Indels 67; Gaps 10;

QY 26 ORKYLKLVK--NYNPLERPANDSQPLTVYFSLSIQIMDVDEKQNVLTTNIWLQSWT 83
DB 27 BEKLMDLLNKTRYNNLIRPATSSQLISKQLSLAQILSNEREQIMTINVWLKQWT 86
QY 84 DHYLQWNVSYPGVKTVPDGOIQWKPDILLYNADSRFDATFTNTVLNVSSGHCVLP 143
DB 87 DYRLTWNSRYEGVNILRIKRIWLPDIVLYNNADGTYESVYTNLIVRSNGSVLWLP 146
QY 144 GIFKSSCYIDVRWFPPDVQHCKLKFSWSYGWSLD--LQMQEADISGYIPNGEWDLVGI 201
DB 147 AIYKSACKIEVKYFPDQQNCTLKFRSWTYDHTIDMVLMFTPTASMODFTFSGEWDVAL 206
QY 202 PKRSERFYCCKEB-YPDVTFVTMMRRRTLYYGLNLIIPCVLISALALLVFLLPADS 260
DB 207 FGRTW----PDPSYVDVYDFIIKRKPLFYINLIIPCVLITLAILVFLPSDCGE 262
QY 261 KISLGITVLLSTTFFMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVTVIVLYVHH 320
DB 263 KMTLCISVLLALTVELLSIKVIPPTSLDVLPIGKYLMTVMVTFSTVTSVCVLNVH 322
QY 321 DPGGKMPKFWTRVILLNWCAWFLBMKRPGEKVRPAOCHKQRCSLASVEMSAVAPPAS 380
DB 323 SPSTHTMAPWRHVLDRIAAILCL---GEQPM-----AHRPATF 360
QY 381 NGNLLYIGFRGLDGVHCVPTPDPSGVVCGRMACSPTHDEHLLHGG-----Q 425
DB 361 QAN-----KTDD-----CSGDLIPAMGNHCHSVGGPQDLEKTPRGCSPL 401
QY 426 PPEGDPDLA--KILEEVRIANFRQCDESEAVCSWEKFAACVVDRICLMAFSVFTIIC 483
DB 402 PPPEASLAVRGLLQELSSLRHFLFKRDMEVAEDWKYVAMVVDRLFLVWFVFCVLGT 461
QY 484 IGLM 488
DB 462 VGLFL 466

CURRENT APPLICATION NUMBER: US/11/037,829A
CURRENT FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US 60/397,380
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 495
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human nACHR alpha4-mouse 5HT3-FLAG chimera
US-11-037-829A-7

Query Match 30.0%; Score 811.5; DB 7; Length 495;
Best Local Similarity 36.1%; Pred. No. 5.7e-67;
Matches 180; Conservative 78; Mismatches 169; Indels 71; Gaps 9;
QY 10 LALAASLL-----HVSLLQSGFQRLKYLKLVNPNLPRPVANDSQPLTVYFSLSLQIMDV 65
DB 17 LLLGTGLLRASSHVEFRAHBERLLKLLPSGYNKWRPVANISDVVLRFGLSIAQLIDV 76
QY 66 DEKNQVLTNNIMLQMSWTHYLOMNVSEYGVKTVRFPDQGIWKPDILLNSADDERFDT 125
DB 77 DEKNQMTTNNVVKQSWHYKLRWDPADYENVTSIRIPSELIWRPDIVLYNNADGFAVT 136
QY 126 FHTNVLVNSGHCQYLPPIGPKSSCIDVRNPPPDVQHKLKEGWSYSGNSLDL--QMQ 183
DB 137 HLTKAHLFDHGRVQMTTPAIYKSSCSIDVTFFPDQDQCTMKFGSWTYDKAKIDLNNMS 196
QY 184 EADISGIVPENGWDLVIGPKSERFVECKEYPDVTFTVTRRTLYYGLNLLIPCVL 243
DB 197 RVDQDFWESGEVIVDAGVTNRYKECAEYDITFAFIRRLPFTTNLIIPCLL 256
QY 244 ISALALLVFLPADSGEKISLGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFASTMI 303
DB 257 ISCLTVLVFLPSECEKILCSVLSLTVFLLLITEIPSTLVIPLIGYFVVCMAL 316
QY 304 VGLSVVTVIVLQYHHDDGGKMPKQWTRVILLNWCAMFLMKRPOEDKVRPACQHKQR 363
DB 317 LVISLAETIFIVRLVHKQDLQRPVDPWLRHLVLDRIAWILCL---GEQPM----- 363
QY 364 CSLASVEMSAVAPPASNGLLYIGRGLDGVHCVTPDPSGVVCGRMACSPTHDEHLHG 423
DB 364 -----AHRPPATFQAN-----KTDD-----CSGSDLLPAMNCHSHV 395
QY 424 G-----QPPEGPDLA--KILBEVRYIANFRQDSEAVCSWEKFAACV 466
DB 396 GGPQDLEKTPRGSGPLPPPREASLAVRGLQLQELSSIRHFLEKRDREMRVARDLVRGV 455
QY 467 VDR-----LCIMAFSV 477
DB 456 LDRLLPRIYLLAVLAYS 473

RESULT 14

US-11-122-144-16
Sequence 16, Application US/11122144
Publication No. US20050287663A1

GENERAL INFORMATION:

APPLICANT: Gillespie, Alison
Claeys, Brian O.
Chavez-Noriega, Laura Elena
Siegel, Robert
Elliott, Kathryn J.

TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
OF NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR, CELLS TRANSFORMED THEREWITH,
AND RECOMBINANT CELL LINE EXPRESSING

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSER: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue

CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/11/122,144
FILING DATE: 04-May-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/703,951
FILING DATE: 01-Nov-2000
APPLICATION NUMBER: US 08/487,596
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kohli, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: SD99511A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3889
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-11-122-144-16
Query Match 28.6%; Score 772; DB 7; Length 458;
Best Local Similarity 33.4%; Pred. No. 2.3e-63;
Matches 162; Conservative 92; Mismatches 151; Indels 80; Gaps 9;
QY 24 BFQRLKYLKLVNPNLPRPVANDSQPLTVYFSLSLQIMDVDEKNQVLTNNIQLMSWT 83
DB 27 ENEDALLRHLFGYQYKQWRPVLSNDTIKVYPLGLKISQLVDVDEKNQVLTNNIQLMSWT 86
QY 84 DHYLQNVSEYGVKTVRFPDQGIWKPDILLNSADDERFDTFTNVLVNSGHCQYLP 143
DB 87 DHKLWNPDDYGGIHSIKVPSESLMPLDVLFPENADGRFEGSLMTKVIVKSNGTVVWTP 146
QY 144 GIFKSSCIDVRNPPPDVQHKLKEGWSYSGNSLDLQ--QEADISGIVPENGWDLV-- 199
DB 147 ASYKSSCTMDVTFPPDRQNCMKFGSWTYDGTWVDLILINENVDRKOPDFDNGEWELNA 206
QY 200 -GIPKRSERFVECKEYPDVTFTVTRRTLYYGLNLLIPCVLSALALLVFLPADS 258
DB 207 KGMKNRRDGVYS-----YPFITYSVLRRLPFLFTLLIIPCLGSLFUTLVVFLPSDE 261
QY 259 GKISLGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIVLQVH 318
DB 262 GKLSLSTVLSVLTFLVIEEIIIPSSKVIPLIGEYLLFTMIFTTSLIIVTVFVINVH 321
QY 319 HHDPDG-GKMPKQWTRVILLNWCAMFLMK-----RPGEDKVRPACQ-----HKQRCSL 366
DB 322 HRSSSTYHPMAPWVKRLFLQKLPKLLCMKDHVDYSSPEKESQPVVVKVLEKKQKQL 381
QY 367 ASVEMSAVAPPASNGNLLYIGRGLDGVHCVTPDPSGVVCGRMACSPTHDEHLHG 426

Db 382 -----SDGEKVLVAF----- 391
QY 427 PEGDPLAKLIEVRVIANFRQDSEAVCEWKEFAACVDRCLCLMAFSVFTIICIGI 486
Db 392 -----LEKAADSIRYISRHVKKEHFISQVQDMKFEVAQVLDRIFLWLFLLI--VSATGSV 443
QY 487 LMSAP 491
Db 444 LIFTP 448
RESULT 15
US-11-122-144-8
; Sequence 8, Application US/11122144
; Publication No. US20050287663A1
; GENERAL INFORMATION:
; APPLICANT: Gillespie, Alison
; Claeps, Brian O.
; Chavez-Noriega, Laura Elena
; Siegel, Robert
; Elliott, Kathryn J.
; TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
; OF NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR, CELLS TRANSFORMED THEREWITH,
; AND RECOMBINANT CELL LINE EXPRESSING
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/11/122,144
; APPLICATION NUMBER: US/11/122,144
; FILING DATE: 04-May-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/703,951
; FILING DATE: 01-Nov-2000
; APPLICATION NUMBER: US 08/487,596
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; APPLICATION NUMBER: US 08/026,031
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohli, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: SD99511A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3889
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-11-122-144-8

Query Match 28.5%; Score 770.5; DB 7; Length 468;
Best Local Similarity 32.7%; Pred. No. 3.2e-63;
Matches 166; Conservative 93; Mismatches 163; Indels 85; Gaps 10;
QY 2 RCSPGGWMLAASLLHVSLOGBFQKLYKBLVKNYNPLERPVANDSQPLTVYFSLSLQ 61
Db 23 RCGLAGAAAGQAQGLSEPSSTAKHEDSLKDLFQDYERWVRPVEHLNDKIKIKFLAISQ 82
QY 62 IMDVDEKNOVLTTNWLQMSWTDHVLQNVSEYPCVKTVRPDPDGOIWKFPDILLYNSADER 121
Db 83 LVDVDEKNQMLTTNWLKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDIVLFNADGR 142
QY 122 PDATHTNVLVNSGHCOYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGGWSLDLQ 181
Db 143 PEGT-STKTVIRYNGTVTWTTPANYKSSCTIDVTFPFDLQNCMKFSGSWYDGSQVDII 201
QY 182 MQEADIS--GYIPNGEWDLVGIPGRKSRFRFYECCKEPPYDVTFVTVMRRRTLYYGLNLLI 239
Db 202 LEDQVDKRDFFDNGEWEIVSATGSGKGNRTDSCCWYPY--VTYSPVIKRLPLFYTLFLII 259
QY 240 PCVLISALALLVFLLPADSGEKISLGITVILSLTTFMLLVAEIMPATSDSVPLIAQYAS 299
Db 260 PCIGLSFLTIVLVFLPSNEGEKICLCTSVLVSALTIVFLVIBIEIIPSSKVIPLIGEYLVF 319
QY 300 TMIIVGLSVVTVIVLQVHHDPDGGKMPKWRVILLNWCWFLRMKRPGBDKVRPACOH 359
Db 320 TMIFTVLSIMVTVFAINHH-----RSSSTH 345
QY 360 KQRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDPDGVGVCMACSPTH--- 416
Db 346 -----NAMAP-----LVKRIF-----LHTLP-----KLLCMRSHVDR 372
QY 417 -----DEHLLHGGOPPEGDPDLAKTILEVRYIANRPRCODESEAVCEWKEFAACVDRCL 472
Db 373 YFTQKEETESGSGPKSSRNTLEAALNSIRYITRHKMKENDRVREVVDWKFTIAQVLDRMFL 432
QY 473 MAFSVFTIICITIGILMSAPNFVEAVSK 499
Db 433 WTFLEVSIVGSLGL-----FVPVIYK 453

Search completed: March 28, 2006, 13:39:00
Job time : 26 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 13:30:14 ; Search time 42 Seconds
(without alignments)
1150.019 Million cell updates/sec

Title: US-10-749-075-2

Perfect score: 2703

Sequence: 1 MRCSPGGVWLAAASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUMP62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2690	99.5	502	1 ACHUA7	nicotinic acetylch
2	2690	99.5	502	2 G02259	alpha 7 neuronal n
3	2545	94.2	502	2 A57175	nicotinic acetylch
4	2331	93.6	502	2 T01378	nicotinic receptor
5	2429	89.9	502	2 JN0113	nicotinic acetylch
6	1816.5	67.2	511	2 JH0173	alpha-bungarotoxin
7	1107.5	41.0	498	2 S68588	nicotinic acetylch
8	1089.5	40.3	560	2 T19622	hypothetical prote
9	998	36.9	461	2 T25671	nicotinic acetylch
10	947	35.0	557	2 S12359	hypothetical prote
11	944	34.9	542	2 T19862	hypothetical prote
12	942.5	34.9	511	2 A40110	nicotinic acetylch
13	938.5	34.7	459	2 S14703	nicotinic acetylch
14	937.5	34.7	528	1 ACCH2N	nicotinic acetylch
15	936.5	34.6	503	2 A53956	nicotinic acetylch
16	935.5	34.6	576	1 ACFFA2	nicotinic acetylch
17	934	34.6	622	1 ACCH4N	nicotinic acetylch
18	933	34.5	502	2 A37040	nicotinic acetylch
19	922	34.1	567	1 ACFFA1	nicotinic acetylch
20	916	33.9	627	2 JC4021	nicotinic acetylch
21	915.5	33.9	495	2 S60589	acetylcholine rece
22	913.5	33.8	625	2 A28456	nicotinic acetylch
23	912	33.7	495	2 B35721	nicotinic acetylch
24	898	33.2	494	2 T09289	nicotinic acetylch
25	895	33.1	517	2 A30992	probable nicotinic
26	887.5	32.8	499	2 A24572	nicotinic acetylch
27	884	32.7	498	2 G02421	nicotinic acetylch
28	877	32.4	521	1 ACFFNN	nicotinic acetylch
29	876.5	32.4	491	1 ACCHNN	nicotinic acetylch

30	876	32.4	470	2 A39218	nicotinic acetylch
31	874	32.3	512	2 B37014	nicotinic acetylch
32	861	31.9	502	2 S10505	nicotinic acetylch
33	857	31.7	457	2 S13872	nicotinic acetylch
34	850	31.4	457	2 A24383	nicotinic acetylch
35	849.5	31.4	511	2 T43634	acetylcholine rece
36	848	31.4	445	2 I49458	nicotinic acetylch
37	845	31.3	457	1 ACBOA1	nicotinic acetylch
38	844.5	31.2	500	2 S12899	nicotinic acetylch
39	842	31.2	457	1 ACHUA1	nicotinic acetylch
40	839	31.0	456	1 ACCHAN	nicotinic acetylch
41	838.5	31.0	503	2 JH0174	hypothetical prote
42	837.5	31.0	468	2 T24724	nicotinic acetylch
43	832.5	30.8	479	2 A55382	nicotinic acetylch
44	829.5	30.7	457	2 S08162	nicotinic acetylch
45	828	30.6	474	2 T27006	hypothetical prote

ALIGNMENTS

RESULT 1

ACHUA7

Nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain

C:Species: Homo sapiens (man)

C>Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 09-Jul-2004

C:Accession: I37185; A54194; S60309

R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.

Mol. Pharmacol. 45, 546-554, 1994

A:Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the Sf9 cells expressed in Xenopus oocytes.

A:Reference number: I37185; MUID:94195283; PMID:8145738

A:Accession: I37185

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-502 <PEN>

A:Cross-references: UNIPROT:P36544; UNIPARC:UPI000016A581; EMBL:X70297; NID:9496606; PID: A:Experimental source: brain neuroblastoma cell line SHSY-5Y

R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.

Genomics 19, 379-381, 1994

A:Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic receptor.

A:Reference number: A54194; MUID:94245214; PMID:8188270

A:Accession: A54194

A:Molecule type: mRNA

A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>

A:Cross-references: UNIPARC:UPI000016A6CF; GB:Z23141; NID:9457736; PID:CAA80672.1; PID: A:Experimental source: retina

C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized C:Genetics:

A:Gene: GDB:CHRNA7

A:Cross-references: GDB:138751; OMIM:118511

A:Map position: 15q14-15q14

A>Note: defects in this gene have been associated with mental retardation and schizophrenia C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains and C:Superfamily: acetylcholine receptor

C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter receptor; F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted F:231-254/Domain: transmembrane #status predicted <TR1>

F:262-280/Domain: transmembrane #status predicted <TR2>

F:296-317/Domain: transmembrane #status predicted <TR3>

F:470-488/Domain: transmembrane #status predicted <TR4>

F:46.90.133/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:150-164/Disulfide bonds: #status predicted

F:365.413/Binding site: phosphate (Ser) (covalent) #status predicted

F:415/Binding site: phosphate (Thr) (covalent) #status predicted

F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match

99.5%; Score 2690; DB 1; Length 502;

Best Local Similarity 99.4%; Pred. No. 2.6e-219;

Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKELVKNNPLERPVANDSQPLTVYFSLSL	60
Db	1	MRCSPGGVWLGAAASLLHVSLOGEFQRLKYLKELVKNNPLERPVANDSQPLTVYFSLSL	60
Qy	61	QIMDVDEKKNQVLTNIWLQMSWDHYLQNNVSEYPGVKTVRPDGOIKWPDILLYNSADE	120
Db	61	QIMDVDEKKNQVLTNIWLQMSWDHYLQNNVSEYPGVKTVRPDGOIKWPDILLYNSADE	120
Qy	121	RFDAFTHTNVLVNSSGHCOYLPPGIFKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDL	180
Db	121	RFDAFTHTNVLVNSSGHCOYLPPGIFKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDL	180
Qy	181	QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDVTFTVMRRRTLYYGLNLLIP	240
Qy	241	CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Db	241	CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Qy	301	MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVRVILLNWCWFLRMKRPGEDEKVRPACQHK	360
Db	301	MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVRVILLNWCWFLRMKRPGEDEKVRPACQHK	360
Qy	361	QRCRLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL	420
Db	361	QRCRLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL	420
Qy	421	LHGGOPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI	480
Db	421	LHGGOPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI	480
Qy	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	
RESULT 2			
G02259			
alpha 7 neuronal nicotinic acetylcholine receptor - human			
C:Species: Homo sapiens (man)			
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004			
C:Accession: G02259			
submitted to the EMBL Data Library, November 1995			
R:Leonard, S.			
A:Reference number: H00936			
A:Accession: G02259			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-502 <LEO>			
A:Cross-references: UNIPROT:P36544; UNIPARC:UPI0000169BDC; EMBL:U40583; NID:g1125076; PI			
C:Superfamily: acetylcholine receptor			
Query Match 99.5%; Score 2690; DB 2; Length 502;			
Best Local Similarity 99.4%; Pred. No. 2.6e-219;			
Matches 499; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKELVKNNPLERPVANDSQPLTVYFSLSL	60
Db	1	MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKELVKNNPLERPVANDSQPLTVYFSLSL	60
Qy	61	QIMDVDEKKNQVLTNIWLQMSWDHYLQNNVSEYPGVKTVRPDGOIKWPDILLYNSADE	120
Db	61	QIMDVDEKKNQVLTNIWLQMSWDHYLQNNVSEYPGVKTVRPDGOIKWPDILLYNSADE	120
Qy	121	RFDAFTHTNVLVNSSGHCOYLPPGIFKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDL	180
Db	121	RFDAFTHTNVLVNSSGHCOYLPPGIFKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDL	180
Qy	181	QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDVTFTVMRRRTLYYGLNLLIP	240

Qy	241	CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Db	241	CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Qy	301	MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVRVILLNWCWFLRMKRPGEDEKVRPACQHK	360
Db	301	MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVRVILLNWCWFLRMKRPGEDEKVRPACQHK	360
Qy	361	QRCRLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL	420
Db	361	QRCRLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL	420
Qy	421	LHGGOPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI	480
Db	421	LHGGOPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI	480
Qy	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	
RESULT 3			
A57175			
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004			
C:Accession: A57175			
R:Orr-Urtreger, A.; Seldin, M.P.; Baldini, A.; Beaudet, A.L.			
Genomics 26, 399-402, 1995			
A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine recept			
A:Reference number: A57175; MUID:95324936; PMID:7601470			
A:Accession: A57175			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-502 <ORR>			
A:Cross-references: UNIPROT:P49582; UNIPARC:UPI000023350D; GB:L37663; NID:g790853; PIDN:1			
C:Superfamily: acetylcholine receptor			
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;			
F:1-23/Domain: signal sequence #status predicted <SIG>			
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predic			
F:231-254/Domain: transmembrane #status predicted <TR1>			
F:262-280/Domain: transmembrane #status predicted <TR2>			
F:296-317/Domain: transmembrane #status predicted <TR3>			
F:470-488/Domain: transmembrane #status predicted <TR4>			
F:46.90.133/Binding site: carbohydrate (Aen) (covalent) #status predicted			
F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted			
F:415/Binding site: phosphate (Thr) (covalent) #status predicted			
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted			
Query Match 94.2%; Score 2545; DB 2; Length 502;			
Best Local Similarity 93.8%; Pred. No. 4.7e-207;			
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;			
Qy	6	GGVWLAALASLLHVSLOGEFQRLKYLKELVKNNPLERPVANDSQPLTVYFSLSLQIMDV	65
Db	6	GGVWLAALASLLHVSLOGEFQRLKYLKELVKNNPLERPVANDSQPLTVYFSLSLQIMDV	65
Qy	66	DEKNQVLTNTNIWLQMSWDHYLQNNVSEYPGVKTVRPDGOIKWPDILLYNSADERPAT	125
Db	66	DEKNQVLTNTNIWLQMSWDHYLQNNVSEYPGVKTVRPDGOIKWPDILLYNSADERPAT	125
Qy	126	FHTNVLVNSSGHCOYLPPGIFKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDLQMOEA	185
Db	126	FHTNVLVNSSGHCOYLPPGIFKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDLQMOEA	185
Qy	186	DISGYIPNGEWDLVGIPGKRSERFYECCKEPYDVTFTVMRRRTLYYGLNLLIPCVLIS	245
Db	186	DISGYIPNGEWDLVGIPGKRSERFYECCKEPYDVTFTVMRRRTLYYGLNLLIPCVLIS	245
Qy	246	ALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG	305
Db	246	ALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG	305

QY 306 LSVVTVTVLVQYHHDDPGCKMPKTRVILLNWCAMFLRMKPGEDKVRPACQHKORRCS 365
DB 306 LSVVTVTVLVRYHHDDPGCKMPKTRVILLNWCAMFLRMKPGEDKVRPACQHKORRCS 365

- QY 366 LASVMSAVAPPASNGNLLYIGFRLDGVCHVPTPDSGVVCGRMACSTPHDEHLHGQ 425
DB 366 LASVELSAGAPPTSNGNLLYIGFRLGEGMHCAFTPDGSGVCGRLACSTPHDEHLHGHTH 425

QY 426 PPEGDDPLAKILIEVRYIANRFRCDSESAVCSWKFAACVVDRLCLMAFSVFTIICITG 485
DB 426 PSDGDDPLAKILIEVRYIANRFRCDSESEVICSEWKFAACVVDRLCLMAFSVFTIICITG 485

QY 486 ILMSAPNFVEAVSKDFA 502
DB 486 ILMSAPNFVEAVSKDFA 502

RESULT 4
T01378
nicotinic receptor alpha 7 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01378
R:Seguela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha 7
A:Reference number: Z14310; MUID:93147931; PMID:7678957
A:Accession: T01378
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <SEG>
A:Cross-references: UNIPROT:Q05941; UNIPARC:UPI0000125244; EMBL:S53987; NID:G2647770; PID
A:Experimental source: brain
C:Superfamily: acetylcholine receptor

Query Match 93.6%; Score 2531; DB 2; Length 502;
Best Local Similarity 93.4%; Pred. No. 7.1e-206;
Matches 464; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 6 GGWTLAALASLHVSLSQGEFQRLKYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
DB 6 GGWTLAALASLHVSLSQGEFQRLKYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65

QY 66 DEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADERFDAT 125
DB 66 DEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKNRFPDQGIWKPDILLYNSADERFDAT 125

QY 126 FHTNVLVNSGHCQYLPPGIPKSSCYIDYRWPFDPVQCKLFGSWSYCGWSLIDLMQEA 185
DB 126 FHTNVLVNASGHCQYLPPGIPKSSCYIDYRWPFDPVQCKLFGSWSYCGWSLIDLMQEA 185

QY 186 DISGYIPNGEWDLVGIPGKRSEPFYECCKEPPDVTFTVMRRRTLYYGLNLLIPCVLIS 245
DB 186 DISSYIPNGEWDLVGIPGKRSEPFYECCKEPPDVTFTVMRRRTLYYGLNLLIPCVLIS 245

QY 246 ALALVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
DB 246 ALALVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305

QY 306 LSVVTVTVLVQYHHDDPGCKMPKTRVILLNWCAMFLRMKPGEDKVRPACQHKORRCS 365
DB 306 LSVVTVTVLVRYHHDDPGCKMPKTRVILLNWCAMFLRMKPGEDKVRPACQHKORRCS 365

QY 366 LASVMSAVAPPASNGNLLYIGFRLDGVCHVPTPDSGVVCGRMACSTPHDEHLHGQ 425
DB 366 LASVELSAGAPPTSNGNLLYIGFRLGEGMHCAFTPDGSGVCGRLACSTPHDEHLHGHTH 425

QY 426 PPEGDDPLAKILIEVRYIANRFRCDSESAVCSWKFAACVVDRLCLMAFSVFTIICITG 485
DB 426 PSDGDDPLAKILIEVRYIANRFRCDSESEVICSEWKFAACVVDRLCLMAFSVFTIICITG 485

QY 486 ILMSAPNFVEAVSKDFA 502
DB 486 ILMSAPNFVEAVSKDFA 502

DB 486 ILMSAPNFVEAVSKDFA 502

RESULT 5
JN0113
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JN0113; JH0172; S28018; B25738; S26566
R:Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.;
Neuron 5, 847-856, 1990
A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentally
A:Reference number: JN0113; MUID:91097796; PMID:1702646
A:Accession: JN0113
A:Molecule type: DNA
A:Residues: 1-502 <COU>
A:Cross-references: UNIPROT:P22770; UNIPARC:UPI0000125243; GB:X68586; NID:G287756; PIDN:
A:Experimental source: white leghorn; brain
R:Schoppa, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAb reveal subtypes of this
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0172
A:Molecule type: mRNA
A:Residues: 1-502 <SCH>
A:Cross-references: UNIPARC:UPI0000125243; EMBL:X52295; NID:G63077; PIDN:CAA36543.1; PID:
A:Experimental source: brain
R:Matter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M.
EMBO J. 11, 4529-4538, 1992
A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter de
A:Reference number: S28018; MUID:93049204; PMID:1425587
A:Accession: S28018
A:Molecule type: DNA
A:Residues: 1-18 <MAS>
A:Cross-references: UNIPARC:UPI0000171278; EMBL:X68246; GB:S49751; NID:G65319; PIDN:CAA4
A:Experimental source: white leghorn; erythrocyte
R:Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; Ra
Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homologous
A:Reference number: A94055; MUID:85270494; PMID:3860855
A:Accession: B25738
A:Molecule type: protein
A:Residues: 24-25, 'E', 28-41, 'X', 43-45, 'X', 47 <CON>
A:Cross-references: UNIPARC:UPI0000177976
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized
C:Genetics:
A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
A:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predic
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-488/Domain: transmembrane #status predicted <TR4>
F:46.90.133/Binding site: carboxylate (Asn) (covalent) #status predicted
F:365.367.413.427.465/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 89.9%; Score 2429; DB 2; Length 502;
Best Local Similarity 90.7%; Pred. No. 3e-197;
Matches 449; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 8 VWLALASLHVSLSQGEFQRLKYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDE 67
DB 8 LWLALASLHVSLSQGEFQRLKYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDE 67

QY 68 KNOVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADERFDATFH 127
DB 68 KNOVLTNNIWLQMSWTDHYLQWNVSEYPGVKNRFPDQGIWKPDILLYNSADERFDATFH 127

QY	128	TNVLNSSGHCQYLPPGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOEADI	187
Db	128	TNVLNSSGHCQYLPPGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOEADI	187
QY	188	SGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLISAL	247
Db	188	SGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLISAL	247
QY	248	ALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLS	307
Db	248	ALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLS	307
QY	308	VVTVTVLQYHHDPDGGKMPKWTVRVILLNWCWFLMRKRPGEDEVKVRPACQHKQRCSLA	367
Db	308	VVTVTVLQYHHDPDGGKMPKWTVRVILLNWCWFLMRKRPGEDEVKVRPACQHKQRCSLS	367
QY	368	SVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDGSGVVCGRMACSPTHDEHLHGQPP	427
Db	368	SVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDGSGVVCGRMACSPTEENLLSHGPPS	427
QY	428	EGDPLAKLIEVRVIANRFRQDSEAVCSWEKFAACVVDRLCLMAFSVFTIICIGIL	487
Db	428	EGDPLAKLIEVRVIANRFRQDSEAEICNWKFAASVVDRLCLMAFSVFTIICIGIL	487
QY	488	MSAPNFVEAVSKDFA 502	
Db	488	MSAPNFVEAVSKDFA 502	
RESULT 6			
JH0173			
alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken			
C:Species: Gallus gallus (chicken)			
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004			
C:Accession: JH0173			
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.			
Neuron 5, 35-48, 1990			
A>Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbS reveal subtypes of this			
A:Reference number: JH0173; PMID:90315158; PMID:2369519			
A:Accession: JH0173			
A:Molecule type: mRNA			
A:Residues: 1-511 <SCH>			
A:Cross-references: UNIPROT:Q03481; UNIPARC:UPI00000FB9BB; GB:X52296; NID:G63081; PIDN:Q			
A:Experimental source: brain			
A>Note: this sequence is similar to acetylcholine receptor alpha chains			
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend			
C:Superfamily: acetylcholine receptor			
C:Keywords: Glycoprotein; transmembrane protein			
F:1-30/Domain: signal sequence #status predicted <SIG>			
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AE			
F:239-262/Domain: transmembrane #status predicted <TM1>			
F:270-288/Domain: transmembrane #status predicted <TM2>			
F:304-323/Domain: transmembrane #status predicted <TM3>			
F:479-496/Domain: transmembrane #status predicted <TM4>			
F:54/Binding site: carbonyl site: carbonyl (Asn) (covalent) #status predicted			
Query Match			
Best Local Similarity 67.2%; Score 1816.5; DB 2; Length 511;			
Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;			
QY	8	VWLAASLLHVSLSQGEFQRLKYLKVNKNPLRPVANDSQPLTVYFSLSLQIMDYDE	67
Db	16	LWASLFLSFFKVSQGESQRLYRDLNRYNRLRPNVNDSPVIVELQSLQIIVDVE	75
QY	68	KNQVLTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDILLNSADERDATH	127
Db	76	KNQVLTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDILLNSADERDATH	135
QY	128	TNVLNSSGHCQYLPPGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOEADI	187
Db	136	TNVLNYSGCCQYIPGILKSTCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOEADI	195
QY	188	SGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLISAL	247

Db	196	SNYISNGEWDLVGVPKGKELYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLISGL	255
QY	248	ALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLS	307
Db	256	ALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLS	315
QY	308	VVTVTVLQYHHDPDGGKMPKWTVRVILLNWCWFLMRKRPGEDEVKVRP-ACQHK--QRRK	364
Db	316	VVTVTVLQYHHDPDGGKMPKWTVRVILLNWCWFLMRKRPGEDEVKVRP-IPKLSCKSYPKHP	374
QY	365	SIASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDGSGVVCGRMACSPTHDEHLHG	424
Db	375	SLKNTMNVLPCHOPSGNMIY-SYHTMENPCPNNDLGSKSGKITCPLSEDEHVKQK	433
QY	425	QPGECDPLAKLIEVRVIANRFRQDSEAVCSWEKFAACVVDRLCLMAFSVFTIICIT	484
Db	434	ALMDTIPVIVKLBSEVQFIAMRFRKQDGEIECSWEKFAAAVVDRLCLVAFLFALICTF	493
QY	485	GILMSAPNFVEAVSKDF 501	
Db	494	TILMSAPNFIEAVSKDF 510	
RESULT 7			
S68588			
nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis e			
C:Species: Caenorhabditis elegans			
C>Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004			
C:Accession: S68588; S57496			
R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.			
J. Mol. Biol. 258, 261-269, 1996			
A>Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.			
A:Reference number: S68587; MUID:96196478; PMID:8627624			
A:Accession: S68588			
A>Status: nucleic acid sequence not shown			
A:Molecule type: mRNA			
A:Residues: 1-498 <BAL>			
A:Cross-references: UNIPROT:P48180; UNIPARC:UPI0000125225; EMBL:X83887; NID:g872087; PID			
C:Superfamily: acetylcholine receptor			
C:Keywords: Glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;			
F:1-19/Domain: signal sequence #status predicted <SIG>			
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT>			
Query Match			
Best Local Similarity 41.0%; Score 1107.5; DB 2; Length 498;			
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;			
QY	10	LALAASLLHVSLSQGEFQ-RKLYKELKVNKNPLRPVANDSQPLTVYFSLSLQIMDVDEK	68
Db	6	LLISCAILAAPTLGLSLQERRUYEDLMRYNNLRPNVANHSEFVTVHLKVALQIIVDEK	65
QY	69	NOVLTNIWLQMSWDHYLQWNVSEYGVKTVRPDQGIWKPDILLNSADERDATH	128
Db	66	NOVTVVNAWLDYTNWYNLVWDKAEYGNITDVRFPAGKIWKPDVLLNSVDNFDSTYT	125
QY	129	NVLNSSGHCQYLPPGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOEAD	186
Db	126	NWIVSTGLVHWVPPGIFKISKIDIQWFPDEQKCFKFGSWTYDGYKLDLPATGQFD	185
QY	187	ISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLISA	246
Db	186	ISEYISNGEWALPLTTVERNEKFYDCCPEYDPDVFHFLHMRRRTLYYGLNIMPICIL	245
QY	247	LALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGL	306
Db	246	MTLLGFTLPDAGEKITLIQITVLLSICFFLSIVSEMSPPTSEAVPLIGIFFTCMIVVTA	305
QY	307	SVWTVTVLQYHHDPDGGKMPKWTVRVILLNWCWFLMRKRPGEDEVKVRPACQHKQRCSL	366
Db	306	STVTVTVVNLHYTFPETHDMPWRNLLWLPWILRMKPG-----HNLTYASL	356
QY	367	ASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPD	412

Db 357 PSU-----PSTKNRHSSELRNIK--DNEHSLSRANSPDACLQNYIMTQSVNSGLTSL 410
QY 413 SPTHDEHLHGQPPGDDP-----LAKILEVRYIANRFRCDSEAVCSWKFAACVW 467
Db 411 GSIPSTMISNGTTDVSQOATLLILRIYHELKIVTKRMIEGDKBEQACNNKFAAMVW 470
QY 468 DRCLCMARSVFTICTIGILMSAPNV 494
Db 471 DRCLYVFTIFIVSTIGIFWAPYLV 497

RESULT 8

T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19622
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: UNIPROT:O62083; UNIPARC:UPI000017799E; EMBL:Z93778; PIDN:CAB07843.1;
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor

Query Match 40.3%; Score 1089.5; DB 2; Length 560;
Best Local Similarity 40.6%; Pred. No. 5.3e-84;
Matches 226; Conservative 93; Mismatches 157; Indels 81; Gaps 9;

QY 10 LALAASLL-----HVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTYVFSLSLQI 62
Db 8 LVLSVSLIWTETKCSKVIWTDGHERRLYAKLAENYKLRPVRNESAVVVLGGDYQOI 67
QY 63 MDVDEKNQVLTNNIQLQMSWTHYLQWNVSEYPGVKTVFPDQGWKPDILLYNSADERF 122
Db 68 LDIDEKHQNMNWMWLMWGTHTLWDESEFNGIKVELPLNNWKPDLVLYNSVDQOF 127
QY 123 DATFTNNVLVNSGHCQYLPFGIFKSSCYIDVRWFPDVQHCKLFGKWSYGGWSLDLQM 182
Db 128 DSTWPNVAVLYTGNVTWIPPAIRSSCAIDYAPFDQCHCTMKFGSWTYSGFDTLIN 187
QY 183 QBADISGYIPNGEWDLVGPGRSERFYECCKEPPDVTFTVMRRRTLYYGNLLIPCV 242
Db 188 TTISPATYKPNGEWELLGLTSQISIPFYECCEPPYDVFTVSIRRTLYYGNLLIPCM 247
QY 243 LLSALALVFLPADSGEKISGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYASTMI 302
Db 248 LLSALLSFTLPADGGEKLNIGVTIFMSLCFMMVAEMPQTSALPLIQIYFSCIMF 307
QY 303 IVGLSVVTVIVLYQHHPDGGK-MPKWTRVILLNWCWFLMRKRPBGDKVRPACQH-- 359
Db 308 QVGASVATVIALNFHRSPEQYKPNKFKTLKLLGWLPTLGMERPDLVELLSVHCAHYA 367
QY 360 -----KORCSLASVEMSAVAPPASNGNLLYTGFRGLD----- 393
Db 368 SDNKKQORYLIEVERHILTRP---NGN---GHSADVKAHVHLDLSTGNPHSDAKKSSPS 420
QY 394 -----GVHCVPFP-----DSGV-----VCGRMACSPTHDEHLLHGQPPGDP---- 431
Db 421 PKRTSASIMGMTGLPTQMNGALDSINKYCTKTVRPLENGSATINHKSSFPQINPINN 480
QY 432 -----DLAKILEEVRYIANRFRCDSEAVCSWKFAACVVDRLCLMAF 475
Db 481 NIYKCANNOKTOPEDRHFHILNELRVISARVRKEEMHALQDMWAFASVDRVUCFLAF 540

QY 476 SVFTIICTIGILMSAPN 492
Db 541 SAFLFWCTAILSYNAPH 557

RESULT 9

T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: UNIPROT:P91197; UNIPARC:UPI00000611B5; EMBL:U88167; PIDN:AAB42223.1;
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 36.9%; Score 998; DB 2; Length 461;
Best Local Similarity 39.8%; Pred. No. 2.2e-76;
Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;

QY 12 LAASLLHVSLL-QGEF-QRKLYKELVKNYNPLRPVANDSQPLTYVFSLSLQIMDVDEKN 69
Db 10 LSLVITHSNLDCGSAETKLTDDLKGNPLRPVQNSQPLKVKIKLFLQQLLDVDEKN 69
QY 70 QVLTNNIQLQMSWTHYLQWNVSEYPGVKTVFP--DGOIWKPDILLYNSADERFDATEPH 127
Db 70 QIVSVNWLSTYTFWPKLQWEPKKYGGIQDIRPFGSSDHIWKPDVLLYNSAAEDFDSIFK 129
QY 128 TNNVLVNSGHCQYLPFGIFKSSCYIDVRWFPDVQHCKLFGKWSYGGWSLDLQM----- 182
Db 130 SNLLTYHTGTVMVIPPVGLKFVCQLDVTWFPDDQVCEMKFGSWTFHGYAIDQLDDDTN 189
QY 193 --QEADISGYIPNGEWDLVGPGRSERFYECCKEPPDVTFTVMRRRTLYYGNLLIP 240
Db 190 GTQSDMLSTYLVNGSMQVISTNAKRVSYKCCPEPYFTVNYLHRRRTLYYGNLLIP 249
QY 241 CVLISALALLVFLPADSGEKISGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 250 SLLISLMAILGFMFPDAGEKITLLEVITLLAIVFPLSWSEMTPTSEAVPLIGVFFSCC 309
QY 301 MIIVGLSVVTVIVLYQHHPDGGKMPKWKTRVILLNWCWFLMRKRPGEDEKVRPACQHK 360
Db 310 MLVVSASVFTIVTLNLHFRSADSHENMPLVRVLEFLPMLLFMSRPGYKFKV----- 363
QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVF-TPDSGVVCGRMACSPTHDEH 419
Db 364 -----ANV-----IDSTDKMPKPKKPNFLDCLNPLSNHAGYEAQ 395
QY 420 LHHGQPPGDPDLAKILEEVRYIANRFRCDSEAVCSWKFAACVVDRLCLMAFVSFT 479
Db 396 ILL-----LHSHVTELRRVAVFAFKESHDRIQTDWRFAAMVVDRACLLLFTVFI 445
QY 480 ICTTIGILMSAPNV 494
Db 446 VISILAIMMSAPHII 460

RESULT 10

S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: S12359
R:Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.; EMBO J. 9, 4391-4398, 1990
A:Title: Sequence and functional expression of a single alpha subunit of an insect nicotinic A:Reference number: S12359; MUID:91092263; PMID:1702381
A:Accession: S12359
A:Molecule type: mRNA
A:Residues: 1-557 <NAR>
A:Cross-references: UNIPROT:P23414; UNIPARC:UPI0000125229; EMBL:X55439; NID:g10133; PIDN C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <NAR>
F:245-266/Domain: transmembrane #status predicted <TM1>
F:274-295/Domain: transmembrane #status predicted <TM2>
F:308-329/Domain: transmembrane #status predicted <TM3>
F:501-523/Domain: transmembrane #status predicted <TM4>
F:47,235/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 35.0%; Score 947; DB 2; Length 557;
Best Local Similarity 37.1%; Pred. No. 5.8e-72;
Matches 201; Conservative 92; Mismatches 177; Indels 72; Gaps 6;

QY 5 PGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVPYFSLSLQIMD 64
Db 6 PPMLLLLLLLLLHPAAANPDARKLYDILLNSYNNELIRPVSNNTDTVLVKGSLRLSOLID 65
QY 65 VDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGKTVRPPDGGQIKWPDILLVNSADERFA 124
Db 66 LNLKQDQILTTNWLSHEWQDKFRWDPAEYGVGTLYVPSEHILWPDVLVYNADGEYV 125
QY 125 TFHTNVLNSGHCQYLPPIGFKSSCYIDVRWFFDVQHKCLKFGWSYGGWSLDLQ--- 181
Db 126 TMTKAVLHHTGKVVWTPPAIFKSSCEIDRVYFPDQOTCFMKFGSWYDGDQIDLKHN 185
QY 182 -----MQEADISGYIPNGEWDLVGIPGRSERFYECCKEPPDVTFTVMTERRTLYY 233
Db 186 QKYDDNKVKVGIDLREYVPSVEWIDLVPAERHEKYPCCAEPPYDIPFNFTLRRKTLFY 245
QY 234 GLNLIPCVLSALALLVFLPADSGEKISIGITVLLSLTTFMLLVASIMPATSDSVPLI 293
Db 246 TVNLIVPCUGISYLSLVFYLPADSGEKIALCISILLSTQTFWFLLSIIISTSLALFLL 305
QY 294 AQYFASTMIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGE--- 350
Db 306 GKYLFTVLVGLSVITIMVLNVHYRKPSTHKMAPVYKVFIRELPKLLMRVPEQLA 365
QY 351 DKVRPACQHKORRCSLASVMSAVAPPPASNGNLLIYIGFRLDGVHCVPPTDPSGVVCGRM 410
Db 366 DLASKRLLRHANHSKLSAAAAAATAASSSS-----AASSPDS--LRHH 408
QY 411 ACSPTHDEHL-LHGGQPPG----- 429
Db 409 LHQHQHQLHLQHLQRPQGGNGLHSANRRGGSAGAFGLPSVVGDLGSLSDVATRKYY 468
QY 430 DPDLAKILEEVRYIANFRCDSESAVCSWKFAACVVDRLCLMAFSVFTIICITGILMS 489
Db 469 PPELEKAIHNVLFIQNHMRQDEFAEDQDQGVFAMVLDRLFLMTIATIASIVGIFAILCE 528
- QY 490 AP 491
Db 529 AP 530

- RESULT 11
T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19862
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188

A:Accession: T19862
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: UNIPROT:Q18556; UNIPARC:UPI000007DC28; EMBL:270266; PIDN:CAA94206.1;
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.2
A:Map position: X
A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 495/
C:Superfamily: acetylcholine receptor

Query Match 34.9%; Score 944; DB 2; Length 542;
Best Local Similarity 37.7%; Pred. No. 1e-71;
Matches 207; Conservative 93; Mismatches 165; Indels 84; Gaps 15;

QY 11 ALAASLLHV-----SLOGEFQKLYKELVKNYNPLERPVANDSOPLTVPYFSLSLQIMDV 65
Db 12 ALHCVLFHLLTEVHSSADEY--RLLDLRLHNYDYPYERPVANASEPLVSVKYLQOQILDV 69
QY 66 DEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGKTVRPPD--GQIWKPDILLVNSADERFD 123
Db 70 DEKNQVLTVAWIEFYQWTDYKLKWDPSYGGIKDIRIPGNANAIWKPDVLLVNSADENFD 129
QY 124 ATFTNVLVNSGHCQYLPPIGFKSSCYIDVRWFFDVQHKCLKFGWSYGGWSLDLQ-- 182
Db 130 STYFVNVVSYTGDVLQVPPGILKLSCKIDITYFPDQIICHLKFGSWTYSGNFIDLRIN 189
QY 183 -----QEADISGYIPNGEWDLVGIPGRSERFYECCKEPPDVTFTVMTERRTLYY 233
Db 190 GPEGKNSIDEGIDVQYVYVQNGEWNLLAVPARHETNIFD--EQYPSLFFYLIIQRTLIY 247
QY 234 GLNLIPCVLSALALLVFLPADSGEKISIGITVLLSLTTFMLLVASIMPATSDSVPLI 293
Db 248 GLNLIIISFLISLMTVLGFTLPDAGEKITLEIILLISVCFSLSVADMTPTSEAVPLI 307
QY 294 -----AQYFASTMIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKR 347
Db 308 GLIIFGAFFSCCLMVWSASVVFVTLVNLNHRKPETHMSPFRLLELLIWLPMILLMR 367
QY 348 PGEDKVRPACQHKORRCSLASVMSAVAPPPASNGNLLIYIG-FRCLDGVHCVPPTDSG-- 404
Db 368 PG--KTIFNCTHLKAEKAEKAKQSSI-----KNG-----VGGPKPTDSVH-----PSEGLS 412
QY 405 -----VVCGR-MACSPTHDEHLHGG-----QPPEGDP----- 431
Db 413 LMKNIKLRQGTIDFEYEFVQHNHMLPVASEMTPRTVYSKVMASVVEDVVMTELNY 472
QY 432 -----DLAKILEEVRYIANFRCDSESAVCSWKFAACVVDRLCLMAFSVFTIICITIG 485
Db 473 MQKACLELKNISSQTRAMRKMEEDERDEQAANDKFAAMVVVDRCLLITFSVFIVVSTCG 532
QY 486 ILMSPNFV 494
Db 533 IMFSSPHLI 541

RESULT 12
A40110
nicotinic acetylcholine receptor alpha-2 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004
C:Accession: A40110
R:Wada, K.; Ballivet, M.; Boulter, J.; Connolly, J.; Wada, E.; Deneris, E.S.; Swanson, L.
Science 240, 330-334, 1988
A:Title: Functional expression of a new pharmacological subtype of brain nicotinic acetyl A:Reference number: A40110; MUID:88178113; PMID:2832952
A:Accession: A40110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <WAD>
A:Cross-references: UNIPROT:P12389; UNIPARC:UPI0000170855; GB:M20297; NID:G202672; PIDN: A:Note: the authors translated the codon TCG for residue 494 as Cys

C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 34.9%; Score 942.5; DB 2; Length 511;
Best Local Similarity 39.0%; Pred. No. 1.2e-71;
Matches 201; Conservative 83; Mismatches 179; Indels 53; Gaps 9;

QY 8 VW--LALASLLVSLQGFQKLYKELVKNYNPLRPVANDSQPLTYVYFSLSLQIMDV 65
DB 16 LMCLLVPAVLTAQQGSHTHAERDLKFLHFGGYNRWARPVNTSDVIVRFGLSIAQLIDV 75
QY 66 DEKNQVLTNTIWLQMSWTDHYLQWNSBYGVKTVRFPDQIQWKPDILLYNADRFQAT 125
DB 76 DEKNQMTTNVWLKQWANDYKLRWDPAEFGNTSLRVPSEMIWIPDIVLYNNADGEFAT 135
QY 126 FHTNVLVNSSGHCQYLPPGIFKSSCYIDVRFPFVQHCKLFGKGSWSYGLSLDLMQOE- 184
DB 136 HMTKAHLPTGTVHWVPPAIYKSSCSIDVTFPPFQDQCKMKFGSWTYDKAKIDLEQMER 195
QY 185 -ADISGYIPNGEWDLVGIPGKSERFYECKEPYDPVTFVTWRRRTLYYGLNLLIPCVL 243
DB 196 TVDLKDYWSGMAIINATGTYNSKKYCCAIYDPVTYFYFIRRLPLEYTNLLIIPCLL 255
QY 244 ISALALLVPLLPADSEKISLGTITVLLSLTTFMLLVABIMPATSDSVPLIAOYFASMTII 303
DB 256 ISCLTVLVYLSGCEGKILCLISVLLSLTVFLLITELIIPSTLSVPLIGYLLFTWLP 315
QY 304 VGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNMCWFLRMKRP-----GEDKVRPA 356
DB 316 VTLSIVTVFVLNVHRSSTHNPWNVVALLGRVPRWLMNRPPLPMELHGSPLDKLS 375
QY 357 COHQKQRCSLASVEMSAVAPPASNGNLYIGRGLDGVCHVCTPDS--GVVCGRMACSP 414
DB 376 PSYHMLETNDAGERETEBEEEDENICV-----CAGLDDSSMGVLYG----- 420
QY 415 THDEHLLHGS-----QPPGEG-----DPLAKILEEYRYIANRFRCODESEAVCS 458
DB 421 -----HGLHLRAMEPTKTPTSQASEILLSPQKALEGVHYIADRURSDADSSVKE 473
QY 459 EWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494
DB 474 DMKYVAVVDRFLWLFIIIVSLFTIGLFL--PPFL 507

RESULT 13
S14703
nicotinic acetylcholine receptor beta-2 chain - goldfish (fragment)
C:Species: Carassius auratus (goldfish)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S14703
R:Hiieber, V.; Bouchev, J.; Agranoff, B.W.; Goldman, D.
Nucleic Acids Res. 18, 5307, 1990
A:Title: Nucleotide and deduced amino acid sequence of the goldfish neural nicotinic acetylcholine receptor
A:Reference number: S14703; MUID:90384858; PMID:2402468
A:Accession: S14703
A:Molecule type: mRNA
A:Residues: 1-459 <HIE>
A:Cross-references: UNIPROT:P19370; UNIPARC:UPI000012526C; EMBL:X54052; NID:G62576; PIDN
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;

Query Match 34.7%; Score 938.5; DB 2; Length 459;
Best Local Similarity 38.5%; Pred. No. 2.4e-71;
Matches 189; Conservative 95; Mismatches 142; Indels 65; Gaps 8;

QY 35 KYNPLRPVANDSQPLTYVYFSLSLQIMDVDEKQVLTNTIWLQMSWTDHYLQWNSBY 94
DB 10 ERYNKLIRPAVNSQVQVITGIKLSLAQLISVNEREQIMTNTYMLAQEWTDYDLVNDPNEY 69
QY 95 PGVKTVPDGOIKWPKDILLYNADRFQATFHTNVLVNSSGHCQVLPPIGFKSSCYIDV 154
DB 70 EGIKKLIRIPSQHLWLPDIVLYNNADGVYFSCNVAVSNTGDIWLPALPYKSAIEV 129

QY 155 RWFPEDVQHCKLFGKGSWSYGLSLDLMQOE--ADISGYIPNGEWDLVGIPGKRSERFYEBC 212
DB 130 RNFPDQDQCKLFGKRSWTYDTELDLVTSFASRDDTTPSGEWDIVSLPGRKNE----- 184
QY 213 CKEP-----YPDVTFTVWRRRTLYYGLNLLIPCVLISALALLVPLPADSGEKISLGTIV 268
DB 185 --DPNDLTVDITVDYFVIRKRPFPYTNIIIPCVLITSLAILVFLYPLSPDCGKVTLCMSV 242
QY 269 LLSLTTFMLLVABIMPATSDSVPLIAOYFASMTIIIVGLSVVTVIVLYQHHDDPGGKMP 328
DB 243 LLALTVFLLISKIVPPTSLAVPLIGKYLMTFVLTSLVTSVCLVNVHRSRSPSTHYP 302
QY 329 KWTRVILLNMCWFLRMKRPCEBDKVRPACQHKORCSLASVEMSAVAPPASNGNLLIYIG 388
DB 303 EMVKCVFLHKLPAFLMRPGRSNVRFRKQKHSFSSHQ----- 344
QY 389 FRGLDGVHCVCTPDSGVVCGRMACSPTHDEHLLHGGQPPG-----DPLAKIL 437
DB 345 ---DGDSPFLTDDPRVCGARV-----GDLPEGSEPRQVRKVRHDQDVDEAI 389
QY 438 BEVRYIANRFRQDSEAVCSEWKPACVDRCLMAFSVFTIICITIGILMSAPNF----- 493
DB 390 DGVRFIAHMKIEDDEGIIEDMKYVAMVIDRFLWLFILVVCVGTGLGVQ-PLFQSYN 448
QY 494 ---VEAVSKDF 501
DB 449 TPVABEYVYGD 459

RESULT 14
ACCH2N
nicotinic acetylcholine receptor alpha-2 chain precursor, neuronal - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S00377
R:Nef, P.; Oneyaer, C.; Alliod, C.; Couturier, S.; Ballivet, M.
EMBO J. 7, 595-601, 1988
A:Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptor subunit families
A:Reference number: S00376; MUID:88283624; PMID:3267226
A:Accession: S00377
A:Molecule type: DNA
A:Residues: 1-528 <NEF>
A:Cross-references: UNIPROT:P09480; UNIPARC:UPI000012522D; EMBL:X07339; NID:G62792; PIDN
C:Genetics:
A:Introns: 21/1; 73/3; 88/3; 125/2; 487/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-528/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <MAT>
F:241-264/Domain: transmembrane #status predicted <TM1>
F:272-290/Domain: transmembrane #status predicted <TM2>
F:306-327/Domain: transmembrane #status predicted <TM3>
F:502-520/Domain: transmembrane #status predicted <TM4>
F:54.104/Binding site: carbohydrate (Aen) (covalent) #status predicted
F:158-172,222-223/Disulfide bonds: #status predicted

Query Match 34.7%; Score 937.5; DB 1; Length 528;
Best Local Similarity 37.8%; Pred. No. 3.4e-71;
Matches 200; Conservative 85; Mismatches 175; Indels 69; Gaps 10;

QY 8 VWLAL---AASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTYVYFSLSLQIMD 64
DB 13 VMCFTVLTQATREQQKPHGFADRLFLKLTFTGYNRWSRPVNTSDVIVKFGLSIAQLID 72
QY 65 VDEKNQVLTNTIWLQMSWTDHYLQWNSBYGVKTVRFPDQIQWKPDILLYNADRFQAT 124
DB 73 VDEKNQMTTNVWLKQWANDYKLRWDPAEFGNTSLRVPSEMIWIPDIVLYNNADGEFAT 132
QY 125 TPTNTVLNVNSSGHCQYLPPIGFKSSCYIDVRFPFVQHCKLFGKGSWSYGLSLDLMQOE 184
DB 133 THMTKAHLFSGKVKVWPPAIYKSSCSIDVTFPPDQDQCKMKFGSWTYDKAKIDLENNE 192
QY 185 --ADISGYIPNGEWDLVGIPGKRSERFYECKEPYDPVTFVTWRRRTLYYGLNLLI 242

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Db      193 HHVDLKDYWGSEWAIINAIGRYSKKYDCCTEYIPDITFFYFVIRRLFLFTINLIIFCL 252
Qy      243 LISALALLVFLPADSGEKISIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFA 298
Db      253 LISLISFLITVLPSPDCGKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIGEYLL 307
Qy      303 IVGLSVVTVIVLYQHHDDPDGGMKPKWTRVILLNWCAMFLMKR-----PGEDKV---- 353
Db      313 FVTLSIIITVFLNVHRSPTSHTPHWVRSFPLGFIPRWLFPMKRPPLLLPAEGTTGOYD 372
Qy      354 RPACQHKQRCSLAS-----VMSAVAPPPASNGNLLYIGRGLDG 394
Db      373 PPGTRLSTSRCLWLETDVDDKWEEEEEEEEEEEEEEKAYPSRPSG-----GSQG 424
Qy      395 VHCVPDPSGVVCGRMACSPTHDEHLLGGQPPE-----GD-----PDLAKILIEE 439
Db      425 TQC-----HYSCERQAGKAS-----GGPAPQVPLKGEVGSQDGLTSPSILRLEG 471
Qy      440 VRYIANRFRQDESBVCSWKFAACVVDRLCLMAFSVFTIICTIGILM 488
Db      472 VQYIADHLRAEDAFSVKEDWKYVAMVIDRIFLWFIIVCLLGTGGLFL 520

RESULT 15
A:3956
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53956; S21338
R:Mihojilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A:Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal
A:Reference number: A53956; MUID:91114756; PMID:1989896
A:Accession: A53956
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-503 <MIH>
A:Cross-references: UNIPROT:P32297; UNIPARC:UPI000016ADF3; GB:M37981; NID:g189252; PIDN:
R:Anand, R.; Lindstrom, J.
submitted to the EMBL Data Library, June 1990
A:Description: Nucleotide sequence of the mature human nicotinic acetylcholine receptor
A:Reference number: S21338
A:Accession: S21338
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 30-503 <ANA>
A:Cross-references: UNIPARC:UPI000016ADAE; EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID
C:Genetics:
A:Gene: GDB:CHRNA3
A:Cross-references: GDB:125219; OMIM:118503
A:Map position: 15q24-15q24
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match      34.6%; Score 936.5; DB 2; Length 503;
Best Local Similarity 37.5%; Pred. No. 3.9e-71;
Matches 191; Conservative 95; Mismatches 167; Indels 57; Gaps 8;

-Qy      4 SPGGV---WLAASLIHVSQGFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
Db      8 AFGAVAPRLLLLSLLPVARASEAHLRFLERFDYNEIIRPVANVSDPVIIHFEVSM 67
Qy      61 QIMVDYKNOVLTTNWLQMSWTDHYLQWNVSEYGVKTVRPDGOIWKPDILLYNSADE 120
Db      68 QLVKVDENVQIMETNLWLKQIWNKYLNWPSDYGABFMRVPQAOKIWKPDIVLYNNAG 127
Qy      121 RFDATFHTNLVNSGHCQYLPFGFKSSCYIDVRWFPPDVQHKLFKGSWSYGGWSLDL 180
Db      128 DFQVDDKTALLKYTGVEVTWIIPAIFKSKCIDVYFFPDYQNCCTWKFGSWYDKAKIDL 187
Qy      181 QM--QEAISGYPNGEWDLVGIPGRSRERFYECCKEYPDVFTVTRRRTLYYGLNLL 238
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Db      188 VLIGSSNWLKDYWGSEWAIKAPGYKHDIKYNCCERIYPDITYSLYIRRLPLFTINLI 247
Qy      239 IPCVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFA 298
Db      248 IPCLLISFLITVLPSPDCGKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIGEYLL 307
Qy      299 STMIIVGLSVVTVIVLYQHHDDPDGGMKPKWTRVILLNWCAMFLMKRPGEDKVRPACQ 358
Db      308 PTMIFVTLSIVITVFLNVHYRTTPTHTMPSWVKTVFLNLLPRVYMFMTRP----- 357
Qy      359 HKQRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPDPS-----GVVCGRMACS 413
Db      358 -----TSNEGNAQKRPPLYGAE-----LSNLCNCSRAESKCKEYPCQDGMCG 401
Qy      414 PTHDEHL-----LHGGOPEG-----DPDLAKILEEVRYIANRFRQDESEA 455
Db      402 YCHHRRIKISNFSANLTRSSSESVDVLSLSALSPEIKAEIQSVKYIAENMKAQNEAKE 461
Qy      456 VCSWKFAACVVDRLCLMAFSVFTIICTIG 485
Db      462 IQDDWKYVAMVIDRIFLW---VFTLVCLIG 488
```

Search completed: March 28, 2006, 13:34:43
Job time : 43 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:26:53 ; Search time 235 Seconds
(without alignments)
1507.129 Million cell updates/sec

Title: US-10-749-075-2

Perfect score: 2703

Sequence: 1 MRCSPGVWLALASLLHVS.....TIGILMSAPNFVEAVSKDPA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	99.8	502	1 ACHA7_HUMAN	P36544 homo sapien
2	2688	99.4	502	2 Q5W554_HUMAN	Q5W554 homo sapien
3	2675	99.0	502	1 ACHA7_MACMU	Q866a2 macaca mula
4	2547	94.2	502	2 Q53YK2_RAT	Q53YK2 rattus norv
5	2546	94.2	502	2 Q9JHD6_MOUSE	Q9Jhd6 mus musculus
6	2545	94.2	502	1 ACHA7_MOUSE	P49582 mus musculus
7	2545	94.2	502	2 Q53YJ9_MOUSE	Q53Yj9 mus musculus
8	2536	93.8	499	1 ACHA7_BOVIN	P54131 bos taurus
9	2531	93.6	502	1 ACHA7_RAT	Q05941 rattus norv
10	2522.5	93.3	531	2 Q5UMH9_RAT	Q5umh9 rattus norv
11	2429	89.9	502	1 ACHA7_CHICK	P22770 gallus gall
12	2073.5	76.7	509	2 Q800C7_BRARE	Q800c7 brachydanio
13	2047.5	75.7	507	2 Q6ZM45_ERARE	Q6zm45 brachydanio
14	1845	68.3	513	2 Q7T2R9_FUGRU	Q7t2r9 fugu rubrip
15	1816.5	67.2	511	2 Q03481_CHICK	Q03481 gallus gall
16	1765.5	65.3	486	2 Q7T2S0_FUGRU	Q7t2s0 fugu rubrip
17	1730	64.0	555	2 Q7T2U0_FUGRU	Q7t2u0 fugu rubrip
18	1725	63.8	592	2 Q4RLA7_TETNG	Q4rla7 tetraodon n
19	1701	62.9	321	2 Q81U24_HUMAN	Q81u24 homo sapien
20	1589.5	58.8	531	2 Q4R1C6_TETNG	Q4r1c6 tetraodon n
21	1574.5	58.3	561	2 Q4SXE7_TETNG	Q4sxe7 tetraodon n
22	1571.5	58.1	554	2 Q7T2T9_FUGRU	Q7t2t9 fugu rubrip
23	1565.5	57.9	474	2 Q7T2U1_FUGRU	Q7t2u1 fugu rubrip
24	1525	56.4	436	2 Q4S7V8_TETNG	Q4s7v8 tetraodon n
25	1450	53.6	456	2 Q4SHG5_TETNG	Q4shg5 tetraodon n
26	1270	47.0	533	2 Q66T30_ANOGA	Q66t30 anopheles g
27	1267	46.9	542	2 Q86MN7_DROME	Q86mn7 drosophila
28	1266.5	46.9	541	2 Q9VMV9_DROME	Q9vmv9 drosophila
29	1265	46.8	808	2 Q7KT97_DROME	Q7kt97 drosophila
30	1264	46.8	560	2 Q7KUV2_DROME	Q7kuv2 drosophila
31	1262	46.7	502	2 Q7Q113_ANOGA	Q7q113 anopheles g

ALIGNMENTS

RESULT 1

ID	ACHA7_HUMAN	STANDARD;	PRT;	502 AA.
AC	P36544; Q15826; Q96RH2; Q99555; Q9BXH0;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-7 subunit precursor.			
GN	Name=CHRNA7; Synonyms=NACHRA7;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEDLINE=94195283; PubMed=8145738;			
RA	Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;			
RT	"Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5Y cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus oocytes".			
RL	Mol Pharmacol. 45:546-554(1994).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Hippocampus;			
RA	Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;			
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=97062879; PubMed=8906617;			
RA	Elliot K.J., Ellis S.B., Berckhan K.J., Urrutia A., Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;			
RT	"Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";			
RL	J. Mol. Neurosci. 7:217-228(1996).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=97162233; PubMed=9009220; DOI=10.1016/S0014-5793(96)01383-X;			
RA	Groot Kormelink P.J., Luyten W.H.M.L.;			
RT	"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32";			
RL	FEBS Lett. 400:309-314(1997).			
RN	[5]			
RP	SEQUENCE REVISION.			
RA	Groot Kormelink P.J., Luyten W.H.M.L.;			
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE.			

32	1262	46.7	509	2	Q66T24_ANOGA	Q66t24 anopheles g
33	1260	46.6	807	2	Q8T7V5_DROME	Q8t7v5 drosophila
34	1254.5	46.4	501	2	Q9XZ14_HELVI	Q9xzi4 heliothis v
35	1247	46.1	490	2	Q66T28_ANOGA	Q66t28 anopheles g
36	1242	45.9	496	2	Q9XZ13_HELVI	Q9xzi3 heliothis v
37	1238	45.8	555	2	Q6RFT1_APIME	Q6rft1 apis mellif
38	1226	45.4	490	2	Q66T26_ANOGA	Q66t26 anopheles g
39	1225	45.3	494	2	Q7KTF9_DROME	Q7ktf9 drosophila
40	1221	45.2	494	2	Q8T7S2_DROME	Q8t7s2 drosophila
41	1219	45.1	494	2	Q9VL79_DROME	Q9vl79 drosophila
42	1217	45.0	494	2	Q86MN8_DROME	Q86mn8 drosophila
43	1217	45.0	508	2	Q6NNY5_DROME	Q6nny5 drosophila
44	1214	44.9	494	2	Q8IPE2_DROME	Q8ipe2 drosophila
45	1214	44.9	494	2	Q8T7S1_DROME	Q8t7s1 drosophila

RC TISSUE=Keratinocyte;
RA Arredondo J., Grando S.A.;
RT "Cloning cholinergic receptors in human keratinocytes."; TAS.
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE OF 17-502.
RC TISSUE=Brain;
RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
RA Lee J., Tian J., Giordano T.;
RT "Cloning and sequence of the human $\alpha 7$ nicotinic acetylcholine
RT receptor.";
RL Drug Dev. Res. 30:252-256(1993).
RN [8]
RP NUCLEOTIDE SEQUENCE OF 24-502.
RC TISSUE=Retina;
RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretto M.,
RA Heinemann S.F.;
RT "Molecular cloning and chromosomal localization of the human $\alpha 7$ -
RT nicotinic receptor subunit gene (CHRNA7).";
RL Genomics 19:379-381(1994).
RN [9]
RP NUCLEOTIDE SEQUENCE OF 118-129.
RX MEDLINE=2181878; PubMed=11829490; DOI=10.1006/geno.2002.6694;
RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
RT "A 3-Mb map of a large segmental duplication overlapping the $\alpha 7$ -
RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
RL Genomics 79:197-209(2002).
RN [10]
RP MASS SPECTROMETRY.
RC TISSUE=Mammary cancer;
RX MEDLINE=21829512; PubMed=11840567;
RX DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database.";
RL Proteomics 2:212-223(2002).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC bungarotoxin. The structure is probably pentameric (By
CC similarity).
CC -!- INTERACTION:
CC P05067:APP; NExp=2; IntAct=EBI-79333, EBI-77613;
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI; RANGE=23-502;
CC NOTE=Ref.10.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X70297; CAA49778.1; -; mRNA.
DR EMBL; U40583; AAB83561.1; -; mRNA.
DR EMBL; U62436; AAB40114.1; -; mRNA.
DR EMBL; Y08420; CAA69697.1; -; mRNA.
DR EMBL; AF385585; AAK68111.1; -; mRNA.
DR EMBL; L25827; -; NOT ANNOTATED CDS; mRNA.
DR EMBL; Z23141; CAA80672.1; -; mRNA.
DR EMBL; AF332758; AAK19515.1; -; Genomic_DNA.
DR PIR; G02259; G02259.
DR PIR; I37185; ACHU7.
DR HSP; P22770; IKL8.
DR IntAct; P36544; -.
DR Ensembl; ENSG00000175344; Homo sapiens.

DR HGNC; HGNC:1960; CHRNA7.
DR MIM; 118511; -.
DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
DR GO; GO:0015464; P:acetylcholine receptor activity; TAS.
DR GO; GO:0004889; P:nicotinic acetylcholine-activated cation-se. .; TAS.
DR GO; GO:0000187; P:activation of MAPK; TAS.
DR GO; GO:0007165; P:signal transduction; NAS.
DR GO; GO:0006810; P:transport; TAS.
DR InterPro; IPR006029; Neu_chan_memb.
DR InterPro; IPR006202; Neu_chan_lig_bd.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR002394; Nic/ace_receptor.
DR PANTHER; PTHR18945; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR PRINTS; PR00254; NICOTINIC.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW Postsynaptic membrane; Signal; Transmembrane; Transport.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 502 Neuronal acetylcholine receptor protein,
FT alpha-7 subunit.
FT TOPO_DOM 23 230 Extracellular (Potential).
FT TRANSMEM 231 255 Potential.
FT TRANSMEM 262 280 Potential.
FT TRANSMEM 296 317 Potential.
FT TOPO_DOM 318 469 Cytoplasmic (Potential).
FT TRANSMEM 470 490 Potential.
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT DISULFID 150 164 By similarity.
FT FT 212 213 Associated with receptor activation (By
FT similarity).
FT CONFLICT 11 11 A -> G (in Ref. 1).
FT CONFLICT 58 58 S -> N (in Ref. 2 and 6).
FT CONFLICT 134 134 S -> P (in Ref. 2 and 6).
FT CONFLICT 364 364 C -> S (in Ref. 8).
FT CONFLICT 375 375 A -> G (in Ref. 1).
FT CONFLICT 409 413 RMACS -> AWPAP (in Ref. 8).
FT SEQUENCE 502 AA; 56449 MW; D94B3A482EAA0E42 CRC64;
SQ
Query Match 99.8%; Score 2698; DB 1; Length 502;
Best Local Similarity 99.8%; Pred. No. 8.4e-213;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALAAASLLHVSILQGEFQRKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAALAAASLLHVSILQGEFQRKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQNNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSGHCQYLPDGI EKSSCYIDVRWPFDDVQHKLKFGSGSYGWSJDL 180
DB 121 RFDATFHTNVLVNSGHCQYLPDGI EKSSCYIDVRWPFDDVQHKLKFGSGSYGWSJDL 180
QY 181 QMQBADI SGYIPNGEWDLVGIPGKRSERFYECCKEPEYDPDVTFTVTRRRRTLYYGLNLLIP 240
DB 181 QMQBADI SGYIPNGEWDLVGIPGKRSERFYECCKEPEYDPDVTFTVTRRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
DB 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLMKRPGEDKVPACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLMKRPGEDKVPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDGSGVVCGRMACSPETHDEHL 420

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Db      361  QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy      421  LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2
Q5W554 HUMAN
ID      Q5W554_HUMAN PRELIMINARY; PRT; 502 AA.
AC      Q5W554;
DT      01-FEB-2005 (TrEMBLrel. 29, Created)
DT      01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT      01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE      Nicotinic acetylcholine alpha-7 subunit.
GN      Name=CHRNA7;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Brain;
RA      Brues M., Bonisch H., Gothert M.;
RT      "Modulatory cannabinoid effects at recombinant homomeric human
RL      nicotinic acetylcholine alpha-7 receptors.";
RL      Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Brain;
RA      Brues M.;
RL      Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
        family.
DR      EMBL; AJ586911; CAE52911.1; -; mRNA.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0045211; C:postsynaptic membrane; IEA.
DR      GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR      GO; GO:0005216; F:ion channel activity; IEA.
DR      GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR      GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; IEA.
DR      GO; GO:0006811; P:ion transport; IEA.
DR      InterPro; IPR006201; Neur_channel.
DR      InterPro; IPR006202; Neur_chan_LBD.
DR      InterPro; IPR006029; Neu_Channel_memb.
DR      InterPro; IPR002394; Nic/ace_receptor.
DR      Pfam; PF02931; Neur_chan_LBD; 1.
DR      Pfam; PF02932; Neur_chan_memb; 1.
DR      PRINTS; PR00254; NICOTINICR.
DR      PRINTS; PR00252; NRIONCHANNEL.
DR      TIGRFAMs; TIGR00860; LIC; 1.
DR      PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW      Ion transport; Ionic channel; Postsynaptic membrane; Transmembrane;
KW      Transport.
SQ      SEQUENCE 502 AA; 56503 MW; 235F80F38FB50F46 CRC64;

Query Match          99.4%; Score 2688; DB 2; Length 502;
Best Local Similarity 99.4%; Pred. No. 5 5e-212;
Matches 499; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  MRCSGGVWLAAASLLHVSQGEFQKLYKELVKYNPLRPVANDSQPLTVYFSLSL 60
Db      1  MRCSGGVWLAAASLLHVSQGEFQKLYKELVKYNPLRPVANDSQPLTVYFSLSL 60
Qy      61  QIMDVDEKNOVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRPDPGQIWKPDILLYNSADE 120

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Db      61  QIMDVDEKNOVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRPDPGQIWKPDILLYNSADE 120
Qy      121  RPDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSNYSYGWSLDL 180
Db      121  RPDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSNYSYGWSLDL 180
Qy      181  QMOEADISGYIENGWDLVGIPGKSERFYECKEPYDPDVTFTVMRRRTLYGLNLLIP 240
Db      181  QMOEADISGYIENGWDLVGIPGKSERFYECKEPYDPDVTFTVMRRRTLYGLNLLIP 240
Qy      241  CVLISALALLVFLPADSGEKISLGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db      241  CVLISALALLVFLPADSGEKISLGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy      301  MIIVGLSVVTVIVLYQHHDDPGGKMPKWTVIIINWCANFLRMKRPGEKVRPACQHK 360
Db      301  MIIVGLSVVTVIVLYQHHDDPGGKMPKWTVIIINWCANFLRMKRPGEKVRPACQHK 360
Qy      361  QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db      361  QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy      421  LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
ACHA7 MACMU
ID      ACHA7 MACMU STANDARD; PRT; 502 AA.
AC      Q866A2;
DT      13-SEP-2005 (Rel. 48, Created)
DT      13-SEP-2005 (Rel. 48, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Neuronal acetylcholine receptor protein, alpha-7 subunit precursor.
GN      Name=CHRNA7;
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC      Cercopithecoidea; Cercopitheciinae; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RX      PubMed=14764638; DOI=10.1210/en.2003-1728;
RA      Proskocil B.J., Sekhon H.S., Jia Y., Savchenko V., Blakely R.D.,
RA      Lindstrom J., Spindel E.R.;
RT      "Acetylcholine is an autocrine or paracrine hormone synthesized and
RT      secreted by airway bronchial epithelial cells.";
RL      Endocrinology 145:2498-2506(2004).
CC      -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC      extensive change in conformation that affects all subunits and
CC      leads to opening of an ion-conducting channel across the plasma
CC      membrane (By similarity).
CC      -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC      bungarotoxin. The structure is probably pentameric (By
CC      similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
        family.
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
DR      EMBL; AF486623; AA084497.1; -; mRNA.
DR      HSSP; P22770; 1KL8.
DR      InterPro; IPR006029; Neu_channel_memb.

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DR InterPro; IPR006202; Neur_chan_lig_bd.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR002394; Nic/ace_receptor.
DR PANTHER; PTHR18945; Neur_chan; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00254; NICOTINIC.
DR PRINTS; PR00252; NRICONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW Postsynaptic membrane; Signal; Transmembrane; Transport.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 502
FT
FT TOPO_DOM 23 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT TOPO_DOM 318 469
FT TRANSMEM 470 490
FT CARBOHYD 46 46
FT CARBOHYD 90 90
FT CARBOHYD 133 133
FT DISULFID 150 164
FT DISULFID 212 213
FT
FT SEQUENCE 502 AA; 56429 MW; 213C8A282242AC4A CRC64;

Query Match 99.0%; Score 2675; DB 1; Length 502;
Best Local Similarity 98.8%; Pred. No. 6.5e-211;
Matches 496; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

QY 1 MRCSPGGWLAALAAALLHVSLOGEFQRLYKELVKNYNPLERPVANDSQPLTVVPSLL 60
Db 1 MRCSPGGWLAALAAALLHVSLOGEFQRLYKELVKNYNPLERPVANDSQPLTVVPSLL 60

QY 61 QIMDVDEKNQVLTNIWLQMSWDHYLQWNSEYFGVKTVPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNIWLQMSWDHYLQWNSEYFGVKTVPDGOIWKPDILLYNSADE 120

QY 121 RPDATFHTNVLVNSGHCQYLPPIGFKSCYIDVRWFFDVQHCCLKFGSWSYGWSL 180
Db 121 RPDATFHTNVLVNSGHCQYLPPIGFKSCYIDVRWFFDVQHCCLKFGSWSYGWSL 180

QY 181 QMOEADISGYIPNGEWDLVGIPGKSEKFEYCKEPEYDVTFTVTRRTLYYGLNLLIP 240
Db 181 QMOEADISGYIPNGEWDLVGIPGKSEKFEYCKEPEYDVTFTVTRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGIITVLLSLTTFMLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGIITVLLSLTTFMLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVVTVIQLYHHDDPGGKMPKWTTRVILLNWCANFLMRKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVVTVIQLYHHDDPGGKMPKWTTRVILLNWCANFLMRKPGEDKVRPACQHK 360

QY 361 QRRCSLASVMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDGSGVVCGRMACSPHDEHL 420
Db 361 QRRCSLASVMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDGSGVVCGRMACSPHDEHL 420

QY 421 LHGGQPPGDPDLAKILLEVRVIANFRQCDESEAVCSWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILLEVRVIANFRQCDESEAVCSWKFACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4
Q53YK2_RAT
_ID Q53YK2_RAT PRELIMINARY; PRT; 502 AA.

AC Q53YK2;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Neuronal nicotinic acetylcholine receptor alpha7 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Groot-Kormelink P.J.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9) family.
DR EMBL; AY574256; AAS90352.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045211; C:postsynaptic membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005226; F:ion channel activity; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane; Transport.
SQ SEQUENCE 502 AA; 56502 MW; 289A30498C7B9A58 CRC64;

Query Match 94.2%; Score 2547; DB 2; Length 502;
Best Local Similarity 93.8%; Pred. No. 2.1e-200;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGVWLAAALAAALLHVSLOGEFQRLYKELVKNYNPLERPVANDSQPLTVVPSLLQIMDV 65
Db 6 GGVWLAAALAAALLHVSLOGEFQRLYKELVKNYNPLERPVANDSQPLTVVPSLLQIMDV 65

QY 66 DEKNQVLTNIWLQMSWDHYLQWNSEYFGVKTVPDGOIWKPDILLYNSADERFPAT 125
Db 66 DEKNQVLTNIWLQMSWDHYLQWNSEYFGVKTVPDGOIWKPDILLYNSADERFPAT 125

QY 126 FHTNVLVNSGHCQYLPPIGFKSCYIDVRWFFDVQHCCLKFGSWSYGWSLQMQEA 185
Db 126 FHTNVLVNSGHCQYLPPIGFKSCYIDVRWFFDVQHCCLKFGSWSYGWSLQMQEA 185

QY 186 DISGYIPNGEWDLVGIPGKSEKFEYCKEPEYDVTFTVTRRTLYYGLNLLIPCVLLIS 245
Db 186 DISGYIPNGEWDLVGIPGKSEKFEYCKEPEYDVTFTVTRRTLYYGLNLLIPCVLLIS 245

QY 246 ALALLVFLPADSGEKISLGIITVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
Db 246 ALALLVFLPADSGEKISLGIITVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305

QY 306 LSVVVTVIQLYHHDDPGGKMPKWTTRVILLNWCANFLMRKPGEDKVRPACQHKRRCS 365
Db 306 LSVVVTVIQLYHHDDPGGKMPKWTTRVILLNWCANFLMRKPGEDKVRPACQHKRRCS 365

QY 366 LASVMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDGSGVVCGRMACSPHDEHLHGQ 425
Db 366 LASVMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDGSGVVCGRMACSPHDEHLHGQ 425

QY 426 PPEGDPDLAKILLEVRVIANFRQCDESEAVCSWKFACVVDRLCLMAFSVFTICTIG 485
Db 426 PPEGDPDLAKILLEVRVIANFRQCDESEAVCSWKFACVVDRLCLMAFSVFTICTIG 485

QY 486 ILSAPNFVEAVSKDFA 502
Db 486 ILSAPNFVEAVSKDFA 502

RESULT 5
Q9JHD6_MOUSE

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ID Q9JHD6_MOUSE PRELIMINARY; PRT; 502 AA.
AC Q9JHD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha 7.
GN Name=Chna7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DBA/2IBg;
RX MEDLINE=97189245; PubMed=9037516; DOI=10.1016/S0169-328X(96)00149-0;
RA Stitzel J.A., Farnham D.A., Collins A.C.;
RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit
RT restriction fragment length polymorphisms with levels of alpha-
RT bungarotoxin binding in brain.";
RL Brain Res. Mol. Brain Res. 43:30-40(1996).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=DBA/2IBg;
RX MEDLINE=97189245; PubMed=9037516; DOI=10.1016/S0169-328X(96)00149-0;
RA Stitzel J.A.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
DR EMBL; AF225980; AAF35885.1; -; mRNA.
DR HSSP; P22770; 1KL8.
DR MGI; MGI:99779; Chna7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_channel_memb.
DR InterPro; IPR002394; Nic/ace_receptor.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00254; NICOTINICR.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRfam; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane; Transport.
KW SEQUENCE 502 AA; 56617 MW; C9353E5136D620E3 CRC64;

Query Match 94.2%; Score 2546; DB 2; Length 502;
Best Local Similarity 93.8%; Pred. No. 2.6e-200;
Matches 466; Conservative 19; Mismatches 12; Indels 0; Gaps 0;

QY 6 GGWTLAALASLLHVSLOGEFORLYKELVKNYNPLRPVANDSQPLTYVFSLLQIMDV 65
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6 GGIWLAALASLLHVSLOGEFORLYKELVKNYNPLRPVANDSQPLTYVFSLLQIMDV 65

QY 66 DEKNQVLTNNIWLQMSWTQHYLQWNSYEPGVKTVRFPDQIWKPDILLYNSADDERFDT 125
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 DEKNQVLTNNIWLQMSWTQHYLQWNSYEPGVKTVRFPDQIWKPDILLYNSADDERFDT 125

QY 126 FHTNLVNSGHCQYLPPIGKFSYCIDVVRFPDFVQHCKLFGKFSWYSGWSLDLQMQEA 185
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 FHTNLVNSGHCQYLPPIGKFSYCIDVVRFPDFVQHCKLFGKFSWYSGWSLDLQMQEA 185

QY 186 DISGYIPNGEWDLVGIPGRSERPFYCKEPPDVDTFTTMRRTLYYGNLLIPCVLIS 245
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
186 DISGYIPNGEWDLVGIPGRSERPFYCKEPPDVDTFTTMRRTLYYGNLLIPCVLIS 245

QY 246 ALALVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASWTMIIVG 305
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
246 ALALVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASWTMIIVG 305

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QY 306 LSVVVTVLVLYQHHDPPGGKMPKWTTRVILLNWCWFLMKPGBDKVRPACQHKORRCS 365
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
306 LSVVVTVLVLYQHHDPPGGKMPKWTTRVILLNWCWFLMKPGBDKVRPACQHKORRCS 365

QY 366 LASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTDHLHGGQ 425
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
366 LASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTDHLHGGQ 425

QY 426 PPEGDPDLAKILEEVRYIANRPRCQDSEAVCSWKFAACVVDRCLCLAFSPFTIICITIG 485
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
426 PPEGDPDLAKILEEVRYIANRPRCQDSEAVCSWKFAACVVDRCLCLAFSPFTIICITIG 485

QY 486 ILMSAPNFVEAVSKDPA 502
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
486 ILMSAPNFVEAVSKDPA 502

RESULT 6
ACHA7_MOUSE
ID ACHA7_MOUSE STANDARD; PRT; 502 AA.
AC P49582;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 subunit precursor.
GN Name=Chna7; Synonyms=Acra7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=95324936; PubMed=7601470;
RA Orr-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.;
RT "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
RT acetylcholine receptor.";
RL Genomics 26:399-402(1995).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC bungarotoxin. The structure is probably pentameric (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

DR EMBL; L37663; AAC42053.1; -; mRNA.
DR PIR; A57175; A57175.
DR HSSP; P22770; 1KL8.
DR Ensemble; ENSMUSG00000030525; Mus musculus.
DR MGI; MGI:99779; Chna7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR006029; Neur_channel_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR002394; Nic/ace_receptor.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00254; NICOTINICR.
DR PRINTS; PR00252; NRIONCHANNEL.

```

DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW Postsynaptic membrane; Signal; Transmembrane; Transport.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 502 Neuronal acetylcholine receptor protein,
FT alpha-7 subunit.
FT TOPO_DOM 23 230 Extracellular (Potential).
FT TRANSMEM 231 255 Potential.
FT TRANSMEM 262 280 Potential.
FT TRANSMEM 296 317 Potential.
FT TOPO_DOM 318 469 Cytoplasmic (Potential).
FT TRANSMEM 470 490 Potential.
FT CARBOHYD 46 46 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc . .) (Potential).
FT DISULFID 150 164 By similarity.
FT DISULFID 212 213 Associated with receptor activation (By similarity).
SQ SEQUENCE 502 AA; 56632 MW; C9312E5226D120E3 CRC64;
Query Match 94.2%; Score 2545; DB 1; Length 502;
Best Local Similarity 93.8%; Pred. No. 3.1e-200;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
QY 6 GGWIALAASLLHVSLSQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
DB 6 GGWIALAASLLHVSLSQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWTDHYLQNMSEYPGVKNVRFDPGQIWKPDILLYNSADRFDAT 125
DB 66 DEKNQVLTNIWLQMSWTDHYLQNMSEYPGVKNVRFDPGQIWKPDILLYNSADRFDAT 125
QY 126 FHTNVLNNSGHCQYLPFGIFKSSCYIDVRPFDPVQHCCKLFGSWSYGGWSLDLQMOEA 185
DB 126 FHTNVLNNSGHCQYLPFGIFKSSCYIDVRPFDPVQHCCKLFGSWSYGGWSLDLQMOEA 185
QY 186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRLTYGLNLLIPCVLIS 245
DB 186 DISSYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRLTYGLNLLIPCVLIS 245
QY 246 ALALVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQVPAFTMIIVG 305
DB 246 ALALVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQVPAFTMIIVG 305
QY 306 LSVVVTIVLVQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVPACQHKPRCS 365
DB 306 LSVVVTIVLVQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVPACQHKPRCS 365
QY 366 LASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHLLHGQ 425
DB 366 LASVELSAGAGPPTSNGNLLYIGFRGLEGMHCAPTDPDSGVVCGRLACSPTHDEHLLHGTH 425
QY 426 PPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFPAACVVDRLCLMAFSVFTIICIG 485
DB 426 PSDGDPDLAKILEEVRYIANRFRQDESEVICSEWKFPAACVVDRLCLMAFSVFTIICIG 485
QY 486 ILMAPNFVEAVSKDFA 502
DB 486 ILMAPNFVEAVSKDFA 502

RESULT 7
Q53YJ9 MOUSE
- ID Q53YJ9_MOUSE PRELIMINARY; PRT; 502 AA.
AC Q53YJ9;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Neuronal nicotinic acetylcholine receptor alpha7 subunit.
GN Name=Chnra7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAUB/c; TISSUE=Brain;
RA Groot-Kormelink P.J.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9) family.
DR EMBL; AY574266; AAS90362.1; -; mRNA.
DR MGI; MGI:99779; Chnra7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane; Transport.
SQ SEQUENCE 502 AA; 56631 MW; C9312E5226D120E3 CRC64;
Query Match 94.2%; Score 2545; DB 2; Length 502;
Best Local Similarity 93.8%; Pred. No. 3.1e-200;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
QY 6 GGWIALAASLLHVSLSQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
DB 6 GGWIALAASLLHVSLSQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWTDHYLQNMSEYPGVKNVRFDPGQIWKPDILLYNSADRFDAT 125
DB 66 DEKNQVLTNIWLQMSWTDHYLQNMSEYPGVKNVRFDPGQIWKPDILLYNSADRFDAT 125
QY 126 FHTNVLNNSGHCQYLPFGIFKSSCYIDVRPFDPVQHCCKLFGSWSYGGWSLDLQMOEA 185
DB 126 FHTNVLNNSGHCQYLPFGIFKSSCYIDVRPFDPVQHCCKLFGSWSYGGWSLDLQMOEA 185
QY 186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRLTYGLNLLIPCVLIS 245
DB 186 DISSYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRLTYGLNLLIPCVLIS 245
QY 246 ALALVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQVPAFTMIIVG 305
DB 246 ALALVFLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQVPAFTMIIVG 305
QY 306 LSVVVTIVLVQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVPACQHKPRCS 365
DB 306 LSVVVTIVLVQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVPACQHKPRCS 365
QY 366 LASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHLLHGQ 425
DB 366 LASVELSAGAGPPTSNGNLLYIGFRGLEGMHCAPTDPDSGVVCGRLACSPTHDEHLLHGTH 425
QY 426 PPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFPAACVVDRLCLMAFSVFTIICIG 485
DB 426 PSDGDPDLAKILEEVRYIANRFRQDESEVICSEWKFPAACVVDRLCLMAFSVFTIICIG 485
QY 486 ILMAPNFVEAVSKDFA 502
DB 486 ILMAPNFVEAVSKDFA 502
RESULT 8
ACHA7 BOVIN
- ID ACHA7_BOVIN STANDARD; PRT; 499 AA.
AC P54131;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 subunit precursor.
GN Name=CHRNA7;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;


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KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane; Transport. 88.6%; Pred. No. 2.3e-198;
SQ SEQUENCE 531 AA; 59746 MW; A8C67E0DE3EFDF47 CRC64;

Query Match 93.3%; Score 2522.5; DB 2; Length 531;
Best Local Similarity 88.6%; Pred. No. 2.3e-198;
Matches 466; Conservative 18; Mismatches 13; Indels 29; Gaps 1;

QY 6 GGWTLAALASLLHVSLOGSFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
DQ 6 GGWTLAALASLLHVSLOGSFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
QY 66 DEKNQVLTNNIWLQMSWTQHYLQMNVSYPGVKTVRFPDQGIWKPDILLNN----- 116
DQ 66 DEKNQVLTNNIWLQMSWTQHYLQMNVSYPGVKTVRFPDQGIWKPDILLNNSCQLHFQ 125
QY 117 -----SADERPDATFHTNVLNVSNGHCQYLPPGIFKSSCYIDVRW 156
DQ 126 DLQNMLREACAQAGDLRVSADERPDATFHTNVLNVSNGHCQYLPPGIFKSSCYIDVRW 185
QY 157 FPFVQVCHCKLFGSWSYGGWSLDLQWQADISGYIPNGEWDLVGPGRKSRFPYECCKEP 216
DQ 186 FPFVQVCHCKLFGSWSYGGWSLDLQWQADISGYIPNGEWDLVGPGRKSRFPYECCKEP 245
QY 217 YPDVTFTVMRRRTLYVGNLIPCVLISALALLVFLPADSGEKLISGITVLLSLTTFM 276
DQ 246 YPDVTFTVMRRRTLYVGNLIPCVLISALALLVFLPADSGEKLISGITVLLSLTTFM 305
QY 277 LLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVTVVIVLYQHHDGDKMPKTRVILL 336
DQ 306 LLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVTVVIVLYQHHDGDKMPKTRVILL 365
QY 337 NWCAMPFLMRKPGEDKVRPAQCHQKRCRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVH 396
DQ 366 NWCAMPFLMRKPGEDKVRPAQCHQKRCRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVH 425
QY 397 CVPTDPSGVVCGMACSPHDEHLHGGOPPGDPLAKILSEVRVIANRFRQDESEAV 456
DQ 426 CAPTDPGSGVVCRLACSPHDEHLHGGOPPGDPLAKILSEVRVIANRFRQDESEVI 485
QY 457 CSEWFAACVDRCLMAFSVFTHIICIGLMSAPNFVEAVSKDPA 502
DQ 486 CSEWFAACVDRCLMAFSVFTHIICIGLMSAPNFVEAVSKDPA 531

RESULT 11
ACHA7 CHICK STANDARD; PRT; 502 AA.
AC P22770;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 subunit precursor.
GN Name=CHRNA7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91097796; PubMed=1702646;
RA Couturier S., Bertrand S., Barak S., Ballivet M.,
RA Millar N., Valera S., Barkas T., Ballivet M.;
RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
RT developmentally regulated and forms a homo-oligomeric channel blocked
RT by alpha-BTX."
RL Neuron 5:847-856(1990).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519; DOI=10.1016/0896-6273(90)90031-A;

RA "Brain alpha-bungarotoxin binding protein cDNAs and MBAs reveal
RT subtypes of this branch of the ligand-gated ion channel gene
RT superfamily."
RL Neuron 5:35-48(1990).
RN
RP NUCLEOTIDE SEQUENCE OF 1-18.
RC STRAIN=White leghorn; TISSUE=Erythrocyte;
RX MEDLINE=93049204; PubMed=1425587;
RA Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,
RA Matter J.M.;
RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
RT promoter develops during morphogenesis of the central nervous
RT system."
RL EMBO J. 11:4529-4538(1992).
RN
RP PROTEIN SEQUENCE OF 24-47.
RC TISSUE=Brain;
RX MEDLINE=85270494; PubMed=3860855;
RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
RA Ray N., Raftery M.A.;
RT "Brain and muscle nicotinic acetylcholine receptors are different but
RT homologous proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
RN
RP MUTAGENESIS OF LEU-270.
RX MEDLINE=92049732; PubMed=1719423; DOI=10.1038/353846a0;
RA Rech F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
RA Husy N., Bertrand S., Ballivet M., Changeux J.-P.;
RT "Mutations in the channel domain alter desensitization of a neuronal
RT nicotinic receptor."
RL Nature 353:846-849(1991).
RN
RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
RX MEDLINE=93024917; PubMed=1383829; DOI=10.1038/359500a0;
RA Galzi J.-L., Devillers-Thiery A., Husy N., Bertrand S.,
RA Changeux J.-P., Bertrand D.;
RT "Mutations in the channel domain of a neuronal nicotinic receptor
RT convert ion selectivity from cationic to anionic."
RL Nature 359:500-505(1992).
CC
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC bungarotoxin. The structure is probably pentameric (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: Alpha-7 transcripts transiently accumulate in
CC the developing optic tectum between E5 and E16.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X68596; CAA48576.1; -; mRNA.
CC EMBL; X52295; CAA36543.1; -; mRNA.
CC EMBL; X68246; CAA48317.1; -; Genomic_DNA.
CC F01; JN0113; JN0113.
CC PDB; 1KL8; NMR; B=201-219.
CC Ensemble; ENSGALG0000004096; Gallus gallus.
CC InterPro; IPR006029; Neur_chan_memb.
CC InterPro; IPR006201; Neur_chan_lig_bd.
CC InterPro; IPR002394; Nic/ace_receptor.
CC PANTHER; PTHR18945; Neur_chan; 1.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
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Db 362 PRSSLSVDLN-ISPQVAQSTNGNLLYIGRGMDDTHYATSPDGSVICSRLVATGEEDV- 419
QY 420 LLHGQGPPE-----GDDPLAKILEVRYIANRPRCODESEAVCSWKFAACVVDRLCLM 473
Db 420 LPGAQASSVSSSGPGGETELSKILDEYRISKFRDQDEEDTVCNWKFAASVIDRLCLM 479
QY 474 AFSVFTICTIGILMSAPNVEAVSKDF 501
Db 480 AFSLFTILCTIGILMSAPNVEAISKDF 507

RESULT 13
Q6ZM45_BRARE
ID Q6ZM45_BRARE PRELIMINARY; PRT; 507 AA.
AC Q6ZM45;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Novel protein similar to mouse and rodent cholinergic receptor,
DE nicotinic, alpha polypeptide 7 (CHRNA7).
GN Name=chna7; Synonyms=OTDARP0000001918; ORFNames=dz70B1.1-001;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Matthews L.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
DR EMBL; AL928677; CAE49579.1; -; Genomic DNA.
DR HSSP; P22770; 1KL8.
DR Ensembl; ENSDARG00000035785; Danio rerio.
DR ZFIN; ZDB-GENE-040108-3; Chrna7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045211; C:postsynaptic membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006029; Neu channel memb.
DR InterPro; IPR006202; Neu chan lig_bd.
DR InterPro; IPR006201; Neu channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00254; NICOTINICR.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane; Transport.
SQ SEQUENCE 507 AA; 57703 MW; 5CD57BC6FA4A3216 CRC64;

Query Match 75.7%; Score 2047.5; DB 2; Length 507;
Best Local Similarity 77.8%; Pred. No. 2.3e-159;
Matches 382; Conservative 49; Mismatches 47; Indels 13; Gaps 5;

QY 19 VSLQGEFQRKLYKELVKNYINPLRPVANDSPQITVYFSLQLQIMDVDEKNOVLTTNIWL 78
Db 20 VSLQGEHQRRLYDLMKDYNPLRPFVFNTHSITVYFSLSLQIMDVDEKNOVLTTNIWL 79
QY 79 QMSWTHYIOMNVSEYVGKTVRPPGQIWKPDILLYNSADRFDAFTFTNVLNVSSGHC 138
Db 80 QLYWYDYQLWNASSEYEGVTNRFPDQIWKPDILLYNSADRFDAFTFTNVLNVSSGAC 139
QY 139 QYLPPGIFKSSCIDVRWPFVQHKLFGSGVSGWISLDLQMQEADISGYIPNGEWDL 198
Db 140 QYLPPGIFKSTCYIDVRWPFPLQRCDLKFGSWTGGWISLDLQMQIDADITGYIANGEWDL 199

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RESULT 14

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Q7T2R9_FUGRU
ID Q7T2R9_FUGRU PRELIMINARY; PRT; 513 AA.
AC Q7T2R9;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Nicotinic acetylcholine receptor alpha 8b subunit (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22859682; PubMed=13679024; DOI=10.1016/S0888-7543(03)00153-8;
RA Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RT Fugu rubripes."
RL Genomics 82:441-451(2003).
CC -1- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
DR EMBL; AY299466; AAP58381.1; -; mRNA.
DR HSSP; P22770; 1KL8.
DR Ensembl; SINFRUG00000139100; Fugu rubripes.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045211; C:postsynaptic membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu Channel memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan memb; 1.
DR PRINTS; PR00254; NICOTINICR.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transport.
NON_TER 1
SQ SEQUENCE 513 AA; 57294 MW; 03315A831E0CA499 CRC64;

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Query Match 68.3%; Score 1845; DB 2; Length 513;
Best Local Similarity 68.5%; Pred. No. 1e-142;
Matches 355; Conservative 47; Mismatches 74; Indels 42; Gaps 7;
QY 20 SLOGEFQRLKYLKELVKNYNPLERPVANDSQPLTVYFSLQLQIMVDKKNQVLTNNIWLQ 79
DB 1 SLOGEQRLKYLKELVKNYNPLERPVANDSQPLTVYFSLQLQIMVDKKNQVLTNNIWLQ 60
QY 80 MSMTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLVNSADERFATFTNNVLSNGHCO 139
DB 61 LYWTIDYLTWNPESYGVQNLRPSPQVWTPDILLVNSADERFATFTNNVLSNAGYICQ 120
QY 140 YLPPGIFKSCYIDVWFPPDQGHCKLFGKSWSYGWSLDLQWQADISGYIPNGEWDIV 199
DB 121 YLPPGILKSTCYIDVWFPPDQGHCKLFGKSWTHNGWMLDLQWLDVDTSTYIPNGEWDIV 180
QY 200 GIPGKSERFYECKEPPYDPDVTFTVMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
DB 181 GVPKRNELYYDCKEPPYDPDVTFTVMRRRTLYYGLNLLIPCVLISGLALLVFLPADSG 240
QY 260 EKISLGITVLLSLTTFMLLVAEIMPATSDVPLIAQYFASMTLIIVGLSVVTVVIVLQYHH 319
DB 241 EKISLGITVLLSLTTFMLLVAEIMPATSDVPLIAQYFASMTLIIVGLSVVTVVIVLQYHH 300
QY 320 HDPDGGKMPKTRVILLNNCAWFLRMKRPCEKVRPA--COR-KORRCSLASVMSAV-- 374
DB 301 HDPHGGKMPKTRVILLNNCAWFLRMKRPCEKVRPA--COR-KORRCSLASVMSAV-- 360
QY 375 -----APPASNGNL--LVIGRGLDGVHCVTPDPSGVVC--GRMACSPHDDH 419
DB 361 LSVPLAQTSGPSCPTGTSNGSMGFYSTVHTDSSCPSPSDSGVALGRNHSPPSE-- 418
QY 420 LLHGGOPPS-----DPLAKTLEVRVIANFRCODESEAVCSWKFA 463
DB 419 ----AEPVGGSGGSLGMGVRVSIPTTILMILAEVSYIAORFQDDEAICSEWKFA 474
QY 464 ACVVDRLCLMAFSVFTIITIGILMSAPNFVAVSKDF 501
DB 475 AAVVDRLCLVAESLSFIITCTILMSAPNFVAVSKDF 512

RESULT 15
Q03481 CHICK PRELIMINARY; PRT; 511 AA.
AC Q03481
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha8 subunit of nicotinic acetylcholine receptor precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Artrosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519; DOI=10.1016/0896-6273(90)90031-A;
- RA Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
RT "Brain alpha-bungarotoxin binding protein cDNAs and Mabs reveal
RT subtypes of this branch of the ligand-gated ion channel gene
RT superfamily."
RL Neuron 5:35-48(1990).
- CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
CC EMBL; X52296; CAA36544.1; -; mRNA.
DR PIR; JH0173; JH0173.
DR HSRP; P22770; 1KL8.
DR Ensembl; ENSGALG00000015336; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045211; C:postsynaptic membrane; IEA.

DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. .; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR InterPro; IPR002394; Nic/ace_receptor.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0254; NICOTINICR.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor; Signal;
KW Transmembrane; Transport.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 511 Potential.
SQ SEQUENCE 511 AA; 58705 MW; 10F362D153EC87A7 CRC64;
Query Match 67.2%; Score 1816.5; DB 2; Length 511;
Best Local Similarity 68.8%; Pred. No. 2.2e-140;
Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;
QY 8 VMLAALSLHVSLOGEFQRLKYLKELVKNYNPLERPVANDSQPLTVYFSLQLQIMVD 67
DB 16 LWASLFLAFFKVSQGESQRLYRDLNLYNPLERPVANDSQPIVVELQLSLQIIDVD 75
QY 68 KNQVLTNNIWLQWNVSEYGVKTVRPPDQGIWKPDILLVNSADERFATPH 127
DB 76 KNQVLTNNIWLQWNVSEYGVKTVRPPDQGIWKPDILLVNSADERFATPH 135
QY 128 TNNVNSGHCOYLPPGIFKSCYIDVWFPPDQGHCKLFGKSWSYGWSLDLQWQAD 187
DB 136 TNNVNSGHCOYLPPGIFKSCYIDVWFPPDQGHCKLFGKSWTHNGWMLDLQWLD 195
QY 188 SGYIPNGEWDIVIGIPKSERFYECKEPPYDPDVTFTVMRRRTLYYGLNLLIPCVL 247
DB 196 SNYISNGEWDIVIGIPKSERFYECKEPPYDPDVTFTVMRRRTLYYGLNLLIPCVL 255
QY 248 ALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDVPLIAQYFASMTLIIVGL 307
DB 256 ALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDVPLIAQYFASMTLIIVGL 315
QY 308 VVTVVIVLQYHHDPDGGKMPKTRVILLNNCAWFLRMKRPCEKVRP--ACOHK--QRRC 364
DB 316 VVTVVIVLQYHHDPDGGKMPKTRVILLNNCAWFLRMKRPCEKVRP--ACOHK--QRRC 374
QY 365 SLASVMSAVAPPPASNGNLVIGRGLDGVHCVTPDPSGVVCGRMACSPTHDEHLLHGG 424
DB 375 SLKNTVMNVLPCHQPSNGNMIY--SVHTMENPCCPNQNDLGSKSGKITCPLSEDNEHVQKK 433
QY 425 QPPEGDPLAKTLEVRVIANFRCODESEAVCSWKFAACVVDRLCLMAFSVFTIICT 484
DB 434 ALMDTIPVIVKILREVQFIAMFRKQDEGEITCSEWKFAAAVIDRLCLVAFTLPAICTF 493
QY 485 GILMSAPNFVAVSKDF 501
DB 494 TILMSAPNFVAVSKDF 510

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